

CC This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of an
 CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease

XX Sequence 9 AA;

Query Match 4.6%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
 Db 1 DFMIQGGDF 9

RESULT 21

AAG68089
 ID AAG68089 standard; peptide; 9 AA.

XX AC AAG68089;

XX XX Homo sapiens.

DT 17-DEC-2001 (first entry)

DE Antitumour peptide cyclophilin B 91-99.

XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.

XX OS Homo sapiens.

PN JP2001245675-A.

PD 11-SEP-2001.

XX 25-DEC-2000; 2000JP-00393047.

PF 28-DEC-1999; 99JP-00374322.

XX (ITOY/) ITO Y.

XX WPI; 2001-610076/70.

PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
 PT lymphocytes and for treating cancer.

XX Claim 8; Page 2; 14pp; Japanese.

XX The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
 CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 CC the above mentioned sequences; and (4) peptides with one or more deleted,
 CC substituted, added or inserted amino acid(s) of the above mentioned
 CC sequences, particularly those having recognising property due to HLA-
 CC A2402 binding CTL, especially having at least 5 amino acids, used for
 CC medicine, particularly anticancer agents, derived from antitumour
 CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 CC genes. The antitumour peptides have cytostatic activities. The peptides
 CC are used for the treatment of cancer. The peptides cause activation of

CC CTL in cancer patients. The present sequence represents a peptide from
 CC the present invention

XX Sequence 9 AA;

Query Match 4.6%; Score 50; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
 Db 1 DFMIQGGDF 9

RESULT 22

ABG79076
 ID ABG79076 standard; peptide; 9 AA.

XX AC ABG79076;

XX 15-NOV-2002 (first entry)

XX Human Cyp-B class I HLA widely expressed antigen peptide #2.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

XX OS Homo sapiens.

XX WO200264057-A2.

XX 22-AUG-2002.

PF 15-FEB-2002; 2002WO-US005212.

XX 15-FEB-2001; 2001US-0268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.

XX Disclosure; Page 17; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,

CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 9 AA;

Query Match 4.6%; Score 50; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
DB 1 DFMIQGGDF 9
|||||
1 DFMIQGGDF 9

RESULT 23
ABR84374
ID ABR84374 standard; peptide; 9 AA.
XX
AC ABR84374;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:24.
XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX JP2002365286-A.
PN
XN 18-DEC-2002.
PD
XX 18-SEP-2001; 2001JP-00283413.
PF
XX 13-NOV-2000; 2000JP-00345094.
PR
XX (ITOY/) ITO Y.
PA
XX WPI; 2003-508315/48.
DR
XX A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
XX The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens;
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 4.6%; Score 50; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
DB 1 DFMIQGGDF 99
|||||
1 DFMIQGGDF 99

RESULT 25
AAI69939
ID AAI69939 standard; peptide; 10 AA.
XX
AC AAI69939;
XX
DT 11-APR-2000 (first entry)
XX

Db 1 DFMIQGGDF 9
|||||
1 DFMIQGGDF 9

RESULT 24
ADC17702
ID ADC17702 standard; peptide; 9 AA.
XX
AC ADC17702;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cyclophilin B protein amino acids 91-99.
XX cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.
XX
OS Synthetic.
XX WO2003020306-A1.
PN
XX 13-MAR-2003.
PD
XX 28-AUG-2002; 2002WO-JP008641.
PF
XX 29-AUG-2001; 2001JP-00260046.
PR
XX (ITOY/) ITOH K.
PA
XX Itoh K, Yamada A;
PI
XX WPI; 2003-300831/29.
DR
XX Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.
XX
PS Claim 8; SEQ ID NO 2; 49pp; Japanese.
XX
XX The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet does not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction or
CC suppressors are also useful for suppressing an allergic reaction to
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 91-99 of the cyclophilin B protein.
XX
SQ Sequence 9 AA;

Query Match 4.6%; Score 50; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
DB 1 DFMIQGGDF 99
|||||
1 DFMIQGGDF 99

RESULT 25
AAI69939
ID AAI69939 standard; peptide; 10 AA.
XX
AC AAI69939;
XX
DT 11-APR-2000 (first entry)
XX

AA69921
ID AAY69921 standard; peptide; 9 AA.
XX
AC AAY69921;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #1.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
FN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
XX WPI; 2000-116932/10.
DR
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 49; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 4.5%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 KFHVRVVKDF 92
DB 1 KFHVRVVKDF 9
RESULT 29
AAB46930
ID AAB46930 standard; peptide; 9 AA.
XX
AC AAB46930;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX

(SUMU) SUMITOMO PHARM CO LTD.
Takasu H, Gotoh M, Yamaoka T;
WPI; 2001-193144/20.
Use of antigenic proteins, peptides, interferon or their encoding DNA, in
the manufacture of an agent for the induction of antigen-specific T
cells.
Disclosure; Page 15; 25pp; English.
This invention describes the novel use of interferons (IFNs) or DNAs
capable of expressing the interferons and/or antigenic proteins (AP),
antigenic peptides derived from the proteins or DNAs capable of
expressing the antigenic proteins or peptides, in the manufacture of an
agent for induction of antigen-specific T cells. The products of the
invention have virucide and cytostatic activity and can be used for gene
therapy or as inducers of antigen-specific T cells. The action of
interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
T cell (CTL) by administering an antigenic peptide in an incomplete
Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
DNA encoding IFNs) are useful in the manufacture of a medicament for
inducing antigen-specific T cells in an individual who has been
administered with AP (or DNA encoding AP) or vice versa. The medicament
is useful for the treatment or prophylaxis of a tumor or a viral
infectious disease
XX
SQ Sequence 9 AA;
Query Match 4.5%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 84 KFHVRVVKDF 92
DB 1 KFHVRVVKDF 9
RESULT 30
AAG68088
ID AAG68088 standard; peptide; 9 AA.
XX
AC AAG68088;
XX
DT 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 84-92.
XX
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
OS Homo sapiens.
XX
PN JP2001245675-A.
XX
PD 11-SEP-2001.
XX
PF 25-DEC-2000; 2000JP-00393047.
XX
PR 28-DEC-1999; 99JP-00374322.
XX
PA (ITOY/) ITO Y.
XX
XX WPI; 2001-610076/70.
XX
PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX

CC The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
 CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 CC the above mentioned sequences; and (4) peptides with one or more deleted,
 CC substituted, added or inserted amino acid(s) of the above mentioned
 CC sequences, particularly those having recognising property due to HLA-
 CC A2402 binding CTL, especially having at least 5 amino acids, used for
 CC medicene, particularly anticancer agents, derived from antitumour
 CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 CC genes. The antitumour peptides have cytostatic activities. The peptides
 CC are used for the treatment of cancer. The peptides cause activation of
 CC CTL in cancer patients. The present sequence represents a peptide from
 CC the present invention

XX Sequence 9 AA;

Query Match 4.5%; Score 49; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 KFHRRVIKDF 92
 |||||
 Db 1 KFHRRVIKDF 9

RESULT 31

ABG79075
 ID ABG79075 standard; peptide; 9 AA.

XX AC ABG79075;

XX DT 15-NOV-2002 (first entry)

XX DE Human Cyp-B class I HLA widely expressed antigen peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

XX OS Homo sapiens.

XX PN WO200264057-A2.

XX PD 22-AUG-2002.

XX PF 15-FEB-2002; 2002WO-US005212.

XX PR 15-FEB-2001; 2001US-0268687P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Wang R;

XX DR WPI; 2002-627577/67.

XX PT Novel composition for treating a disease in an animal, comprises an
 XX immune effector cell and cell penetrating peptide associated with an
 XX antigen or antibody.

XX PS Disclosure; Page 17; 6lpp; English.

XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-

CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention

XX Sequence 9 AA;

Query Match 4.5%; Score 49; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 KFHRRVIKDF 92
 |||||
 Db 1 KFHRRVIKDF 9

RESULT 32

ABR84373

ID ABR84373 standard; peptide; 9 AA.

XX AC ABR84373;

XX DT 06-NOV-2003 (first entry)

XX DE Human CypB HLA-A24 epitope, SEQ ID NO:23.

XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 KW human; human leukocyte antigen; HLA-A24 epitope.

XX OS Homo sapiens.

XX PN JP2002365286-A.

XX PD 18-DEC-2002.

XX PF 18-SEP-2001; 2001JP-00283413.

XX PR 13-NOV-2000; 2000JP-00345094.

XX PA (ITOY/) ITO Y.

XX DR WPI; 2003-508315/48.

XX A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.

XX Example 8; Page 10; 18pp; Japanese.

XX The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens;
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate

CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention

XX Sequence 9 AA;

Query Match 4.5%; Score 49; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 KHRVVIKDF 92
 DB 1 KHRVVIKDF 9

RESULT 33
 ADCL17701
 ID ADCL17701 standard; peptide; 9 AA.

XX AC ADCL17701;

XX DT 18-DEC-2003 (first entry)

XX DE Cyclophilin B protein amino acids 84-92.

XX KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.

XX OS Synthetic.

XX PN WO2003020306-A1.

XX PD 13-MAR-2003.

XX PF 28-AUG-2002; 2002WO-JP008641.

XX PR 29-AUG-2001; 2001JP-00260046.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Yamada A;

XX PS WPI; 2003-300831/29.

XX PT Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.

XX PS Claim 8; SEQ ID NO 1; 49pp; Japanese.

XX CC The invention relates to allergic reaction suppressors, comprising a
 CC peptide which originates from the same antigenic substance as the
 CC antigenic substance inducing the (peptide-originated) allergic reaction,
 CC and containing an epitope different from the epitope participating in the
 CC induction of the allergic reaction and yet does not induce the allergic
 CC reaction. The desensitizers or allergic reaction suppressors are useful
 CC for treating and preventing type I allergic diseases and in cancer
 CC vaccines for preventing or treating cancer. The allergic reaction or
 CC suppressors are also useful for suppressing an allergic reaction or
 CC reducing immunoglobulin E antibody production, and for desensitization to
 CC antigens. This sequence represents a peptide used in the invention and
 CC corresponds to amino acids 84-92 of the cyclophilin B protein.

XX Sequence 9 AA;

Query Match 4.5%; Score 49; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 KHRVVIKDF 92
 DB 1 KHRVVIKDF 9

RESULT 34

AAV69950
 ID AAV69950 standard; peptide; 8 AA.

XX AC AAV69950;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #30.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9567288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.

XX PS Claim 4; Page 57; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 8 AA;

Query Match 4.4%; Score 48; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 WLDGRHVV 160
 DB 1 WLDGRHVV 8

RESULT 35

AAV72947

ID AAV72947 standard; peptide; 14 AA.

XX AC AAV72947;

XX DT 16-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 29-NOV-1995 (first entry)

XX DE E. coli PPIase-alpha tryptic fragment 4.

XX KW Escherichia coli; protein conformation; folding; acceleration;

XX KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;

XX KW isomerisation; prolyl peptide bond.

XX OS Escherichia coli; (ST 249 strain).

```

XX EP647714-A1.
XX PN
XX PD
XX 12-APR-1995.
XX PF
XX 19-JUL-1990; 94EP-00203612.
XX PR
XX 19-JUL-1989; 89JP-00184738.
XX PR
XX 06-OCT-1989; 89JP-00260244.
XX PR
XX 29-DEC-1989; 89JP-00344705.
XX PR
XX 19-JUL-1990; 90EP-00307914.
XX XX
XX (TOFU ) TONEN CORP.
XX PI
XX Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX WI; 1995-140756/19.
XX DR
XX
XX
XX New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate
PT the folding of proteins, partic. for activation of inactive recombinant
PT proteins.
XX
XX Example 7; Page 30; 85pp; English.
XX
XX AAR72900-04 are tryptic fragments of E. coli PPIase-alpha (peptidyl
CC prolyl cis trans isomerase). The E. coli PPIase-beta has a single mol.
CC wt. of about 22 kDa and a single isoelectric point of about 9.7. The
CC enzyme catalyses the isomerisation of prolyl peptide bonds in proteins
CC and accelerates the folding of the protein. The inventors are claiming
CC the PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 14 AA;
XX
XX Query Match 4.4%; Score 48; DB 2; Length 14;
XX Best Local Similarity 76.9%; Pred. No. 3.9e+02;
XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 88 VIKDFMIQGGDFT 100
XX || || || || || || ||
XX 1 VIPGFMIQGGGFT 13
XX
XX
XX RESULT 37
XX AAY69963
XX ID AAY69963 standard; peptide; 9 AA.
XX AC
XX AAY69963;
XX XX
XX 11-APR-2000 (first entry)
XX
XX Human cyclophilin B peptide fragment #43.
XX
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
XX
XX WO9967288-A1.
XX PN
XX 29-DEC-1999.
XX PD
XX
XX 24-JUN-1999; 99WO-JP003360.
XX PF
XX
XX 25-JUN-1998; 98JP-00178449.
XX PR
XX
XX (SUMU ) SUMITOMO PHARM CO LTD.
XX PA
XX (ITOH/) ITOH K.
XX
XX Itch K, Gomi S;
XX PI
XX
XX WPI; 2000-116932/10.
XX DR
XX
XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
XX Claim 10; Page 60; 64pp; Japanese.
XX PS
XX
XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 4.4%; Score 48; DB 2; Length 14;
XX Best Local Similarity 76.9%; Pred. No. 3.9e+02;
XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 88 VIKDFMIQGGDFT 100
XX || || || || || || ||
XX 1 VIPGFMIQGGGFT 13
XX
XX
XX RESULT 36
XX AAR72903
XX ID AAR72903 standard; peptide; 14 AA.
XX AC
XX AAR72903;
XX XX
XX 16-OCT-2003 (revised)
XX DT
XX 25-MAR-2003 (revised)
XX DT
XX 29-NOV-1995 (first entry)
XX
XX E. coli PPIase-alpha tryptic fragment 4.
XX
XX Escherichia coli; protein conformation; folding; acceleration;
KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KW isomerisation; prolyl peptide bond.
XX
XX Escherichia coli; (ST 249 strain).
XX OS
XX
XX EP647713-A1.
XX PN
XX
XX 12-APR-1995.
XX PD
XX
XX 19-JUL-1990; 94EP-00203610.
XX PF
XX
XX 19-JUL-1989; 89JP-00184738.
XX PR
XX 06-OCT-1989; 89JP-00260244.
XX PR
XX 29-DEC-1989; 89JP-00344705.
XX PR
XX 19-JUL-1990; 90EP-00307914.
XX PR
XX
XX

```

Query Match 4.3%; Score 47; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
|:|||||||
Db 1 DYMIQGGDF 9

RESULT 38

AAB46947
ID AAB46947 standard; peptide; 9 AA.

XX AC AAB46947;

XX DT 04-MAY-2001 (first entry)

XX DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.

XX KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;

XX KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;

XX KW viral infectious disease; cyclophilin B; human.

XX OS Homo sapiens.

XX PN EP1074267-A1.

XX PD 07-FEB-2001.

XX PF 24-JUL-2000; 2000EP-00306263.

XX PR 22-JUL-1999; 99JP-00207687.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PI Takasu H, Gotoh M, Yamaoka T;

XX DR WPI; 2001-193144/20.

XX PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in the manufacture of an agent for the induction of antigen-specific T cells.

XX PS Disclosure; Page 20; 25pp; English.

CC This invention describes the novel use of interferons (IFNs) or DNAs capable of expressing the interferons and/or antigenic proteins (AP), antigenic peptides derived from the proteins or DNAs capable of expressing the antigenic proteins or peptides, in the manufacture of an agent for induction of antigen-specific T cells. The products of the invention have virucide and cytostatic activity and can be used for gene therapy or as inducers of antigen-specific T cells. The action of interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic T cell (CTL) by administering an antigenic peptide in an incomplete Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or DNA encoding IFNs) are useful in the manufacture of a medicament for inducing antigen-specific T cells in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament is useful for the treatment or prophylaxis of a tumor or a viral infectious disease

XX Sequence 9 AA;

Query Match 4.3%; Score 47; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
|:|||||||
Db 1 DYMIQGGDF 9

RESULT 39

ADCL17709
ID ADCL17709 standard; peptide; 9 AA.

XX AC ADCL17709;

XX DT 18-DEC-2003 (first entry)

XX DE Modified cyclophilin B protein amino acids 91-99.

XX KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen; allergy; epitope; cancer; immunoglobulin E antibody; desensitization; cyclophilin B.

XX OS Synthetic.

XX PN WO2003020306-A1.

XX PD 13-MAR-2003.

XX PF 28-AUG-2002; 2002WO-UP008641.

XX PR 29-AUG-2001; 2001JP-00260046.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Yamada A;

XX DR WPI; 2003-300831/29.

XX PT Desensitizers or allergic reaction suppressors containing peptides originating from the same antigenic substances as reaction-inducing PT substances, useful for preventing or treating type I allergic diseases and in cancer vaccines.

XX PS Claim 8; SEQ ID NO 9; 49pp; Japanese.

XX CC The invention relates to allergic reaction suppressors, comprising a peptide which originates from the same antigenic substance as the antigenic substance inducing the (peptide-originated) allergic reaction, and containing an epitope different from the epitope participating in the induction of the allergic reaction and yet does not induce the allergic reaction. The desensitizers or allergic reaction suppressors are useful for treating and preventing type I allergic diseases and in cancer vaccines for preventing or treating cancer. The allergic reaction or suppressors are also useful for suppressing an allergic reaction or reducing immunoglobulin E antibody production, and for desensitization to antigens. This sequence represents a peptide used in the invention and corresponds to amino acids 91-99 of the cyclophilin B protein with the Phe at position 92 replaced by a Tyr.

XX SQ Sequence 9 AA;

Query Match 4.3%; Score 47; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
|:|||||||
Db 1 DYMIQGGDF 9

RESULT 40

AAV69962

ID AAV69962 standard; peptide; 9 AA.

XX AC AAV69962;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #42.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.
 XX OS Homo sapiens.
 XX PN WO9967288-A1.
 XX XX 29-DEC-1999.
 PD XX
 XX PF 24-JUN-1999; 99WO-JP003360.
 XX XX
 XX PR 25-JUN-1998; 98JP-00178449.
 XX XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX XX
 PI Itoh K, Gomi S;
 XX XX
 DR WPI; 2000-116932/10.
 XX XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX XX
 PS Claim 10; Page 60; 64pp; Japanese.
 XX XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX XX
 SQ Sequence 9 AA;
 Query Match 4.2%; Score 46; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 84 KFHRYIKDF 92
 Db :|||||
 1 KYHRVIRKDF 9
 RESULT 41
 AAY69941
 ID AAY69941 standard; peptide; 9 AA.
 XX AC
 XX AC AAY69941;
 XX DT 11-APR-2000 (first entry)
 XX DE Human cyclophilin B peptide fragment #21.
 XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX XX
 OS Homo sapiens.
 XX PN WO9967288-A1.
 XX PD 29-DEC-1999.
 XX PF 24-JUN-1999; 99WO-JP003360.
 XX XX
 XX PR 25-JUN-1998; 98JP-00178449.
 XX XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX XX
 PI Itoh K, Gomi S;
 XX XX
 DR WPI; 2000-116932/10.
 XX XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX XX

PS Claim 4; Page 55; 64pp; Japanese.
 XX XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX XX
 SQ Sequence 9 AA;
 Query Match 4.2%; Score 46; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 DLRIQDEDEV 49
 Db :|||||
 1 DLRIQDEDEV 9
 RESULT 42
 AAB46946
 ID AAB46946 standard; peptide; 9 AA.
 XX AC
 XX AC AAB46946;
 XX DT 04-MAY-2001 (first entry)
 XX DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
 XX KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
 KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 KW viral infectious disease; cyclophilin B; human.
 XX OS Homo sapiens.
 XX XX
 XX EP1074267-A1.
 XX PD 07-FEB-2001.
 XX XX
 XX PF 24-JUL-2000; 2000EP-00306263.
 XX PR 22-JUL-1999; 99JP-00207687.
 XX XX
 XX (SUMU) SUMITOMO PHARM CO LTD.
 XX XX
 XX Takasu H, Gotoh M, Yamaoka T;
 XX DR WPI; 2001-193144/20.
 XX XX
 PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
 PT the manufacture of an agent for the induction of antigen-specific T
 PT cells.
 XX XX
 PS Disclosure; Page 19; 25pp; English.
 XX XX
 CC This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of an
 CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease
 XX XX
 SQ Sequence 9 AA;
 Query Match 4.2%; Score 46; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 84 KPHRVIKDF 92
|:|||||
Db 1 KYHRVIKDF 9

RESULT 43
AAY69937
ID AAY69937 standard; peptide; 10 AA.

XX AC AAY69937;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #17.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.

XX PS Claim 4; Page 53; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;

Query Match 4.2%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LIAGSVFFLL 18
|:|||||
Db 1 LIAGSVFFLL 10

RESULT 44
AAY69934
ID AAY69934 standard; peptide; 10 AA.

XX AC AAY69934;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #14.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.

XX PS Claim 4; Page 53; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;

Query Match 4.2%; Score 46; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALIAGSVFFL 17
|:|||||

Db 1 ALIAGSVFFL 10

RESULT 45
AAY69933
ID AAY69933 standard; peptide; 11 AA.

XX AC AAY69933;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #13.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.

XX PS Claim 4; Page 52; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The

CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX

SQ Sequence 11 AA;

Query Match 4.2%; Score 46; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LLAALIAAGSV 14
 |||||
 Db 1 LLAALIAAGSV 11

Search completed: August 30, 2004, 10:49:40
 Job time : 309.892 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 16,3885 Seconds

(without alignments)
189.846 Million cell updates/sec

Title: US-09-720-469A-4
Perfect score: 60
Sequence: 1 GYKNSKPHRVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	3 AAY69924	Aay69924 Human cyp
2	39	65.0	9	3 AAY69923	Aay69923 Human cyp
3	32	53.3	9	3 AAY69921	Aay69921 Human cyp
4	32	53.3	9	4 AAB46930	Aab46930 Human cyp
5	32	53.3	9	4 AAG68088	Aag68088 Antitumou
6	32	53.3	9	5 ABG79075	Abg79075 Human cyp
7	32	53.3	9	6 ABR84373	Abr84373 Human cyp
8	32	53.3	9	7 ADC17701	Adc17701 Cyclophil
9	30	50.0	11	2 AAR72931	Aar72931 E. coli p
10	30	50.0	11	2 AAR72887	Aar72887 E. coli p
11	29	48.3	9	3 AAY69962	Aay69962 Human cyp
12	29	48.3	9	4 AAB46946	Aab46946 Human cyp
13	29	48.3	10	3 AAB27129	Aab27129 Human CAS
14	28	46.7	9	2 AAW33943	Aaw33943 Betal-adr
15	28	46.7	14	2 AAW33942	Aaw33942 Betal-adr
16	28	46.7	14	5 ABJ15069	Abj15069 Human 125
17	27	45.0	9	3 AAY69959	Aay69959 Human cyp
18	27	45.0	9	7 ABR84746	Abr84746 Bovine po
19	27	45.0	11	7 ADD88599	Add88599 Influenza
20	26.5	44.2	11	2 AAW19409	Aaw19409 Anti-fung
21	26.5	44.2	11	2 AAW19455	Aaw19455 Anti-fung
22	26.5	44.2	12	2 AAW19415	Aaw19415 Anti-fung
23	26.5	44.2	12	2 AAW19417	Aaw19417 Anti-fung
24	26.5	44.2	12	2 AAW19414	Aaw19414 Anti-fung
25	26.5	44.2	12	2 AAW19407	Aaw19407 Anti-fung

26	26.5	44.2	12	2	AAW19426	Anti-fung
27	26.5	44.2	12	2	AAW19454	Anti-fung
28	26.5	44.2	12	2	AAW19461	Anti-fung
29	26.5	44.2	12	2	AAW19460	Anti-fung
30	26.5	44.2	12	2	AAW19463	Anti-fung
31	26.5	44.2	12	2	AAW19472	Anti-fung
32	26.5	44.2	12	2	AAW25141	Antibacte
33	26.5	44.2	12	2	AAW25143	Antibacte
34	26.5	44.2	12	2	AAW25140	Antibacte
35	26.5	44.2	12	3	AAW11990	Histatin-
36	26.5	44.2	12	3	AAW11976	Histatin-
37	26.5	44.2	12	3	AAW11985	Histatin-
38	26.5	44.2	12	3	AAW11987	Histatin-
39	26.5	44.2	12	3	AAW11977	Histatin-
40	26.5	44.2	12	7	ADB81288	Biologica
41	26.5	44.2	14	2	AAR89887	Human his
42	26.5	44.2	14	2	AAW19441	Anti-fung
43	26.5	44.2	14	2	AAW19452	Anti-fung
44	26.5	44.2	14	2	AAW31675	Human his
45	26	43.3	9	2	AAW49599	Human leu

ALIGNMENTS

RESULT 1
AAY69924
ID AAY69924 standard; peptide; 11 AA.
XX AC AAY69924;
XX AC
XX 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #4.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX XX
XX WO9967288-A1.
XX 29-DEC-1999.
XX PD
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.
XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.
XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 50; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 60; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNSKPHRVI 11
|||||||

```

Db      1 GYKNSKPHRVI 11

RESULT 2
AAV69923
ID AAV69923 standard; peptide; 9 AA.
XX
AC AAV69923;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #3.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN W09967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI ITOH/ ITOH K.
XX
PI Itoh K, Gomi S;
XX
WPI; 2000-116932/10.
XX
Tumor antigen peptides derived from cyclophilin B for treatment and
diagnosis of tumors.
XX
Claim 4; Page 49; 64pp; Japanese.
XX
This sequence represents a cyclophilin B peptide of the invention. The
peptides are tumour antigen peptides derived from cyclophilin B, that
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 53.3%; Score 32; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 KPHRVI 11
DB 1 KPHRVI 6

RESULT 4
AAB46930
ID AAB46930 standard; peptide; 9 AA.
XX
AC AAB46930;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
PN EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
WPI; 2001-19344/20.
XX
Use of antigenic proteins, peptides, interferon or their encoding DNA, in
the manufacture of an agent for the induction of antigen-specific T
cells.
XX
Disclosure; Page 15; 25pp; English.
XX
This invention describes the novel use of interferons (IFNs) or DNAs
capable of expressing the interferons and/or antigenic proteins (AP),
antigenic peptides derived from the proteins or DNAs capable of
expressing the antigenic proteins or peptides, in the manufacture of an
agent for induction of antigen-specific T cells. The products of the

```

```

Db      1 GYKNSKPHRVI 11

RESULT 3
AAV69921
ID AAV69921 standard; peptide; 9 AA.
XX
AC AAV69921;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #1.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN W09967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI ITOH/ ITOH K.
XX
PI Itoh K, Gomi S;
XX
WPI; 2000-116932/10.
XX
Tumor antigen peptides derived from cyclophilin B for treatment and
diagnosis of tumors.
XX
Claim 4; Page 50; 64pp; Japanese.
XX
This sequence represents a cyclophilin B peptide of the invention. The
peptides are tumour antigen peptides derived from cyclophilin B, that
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 65.0%; Score 39; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYKNSKF 7
DB 3 GYKNSKF 9

RESULT 3
AAV69921
ID AAV69921 standard; peptide; 9 AA.
XX
AC AAV69921;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #1.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN W09967288-A1.
XX
PD 29-DEC-1999.
XX

```

CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease

XX SQ Sequence 9 AA;

Query Match 53.3%; Score 32; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFHRI 11
 DB 1 KFHRI 6
 |||||

RESULT 5
 AAG68088
 ID AAG68088 standard; peptide; 9 AA.

XX AC AAG68088;

XX DT 17-DEC-2001 (first entry)

XX DE Antitumour peptide cyclophilin B 84-92.

XX KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.

XX OS Homo sapiens.

XX XX JP2001245675-A.

XX PD 11-SEP-2001.

XX PF 25-DEC-2000; 2000JP-00393047.

XX PR 28-DEC-1999; 99JP-00374322.

XX PA (ITOY/) ITO Y.

XX DR WPI; 2001-610076/70.

XX XX New peptides for recognizing cancer cells with tumor specific cytotoxic T

PT lymphocytes and for treating cancer.

PS Claim 8; Page 2; 14pp; Japanese.

CC The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
 CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 CC the above mentioned sequences; and (4) peptides with one or more deleted,
 CC substituted, added or inserted amino acid(s) of the above mentioned
 CC sequences, particularly those having recognising property due to HLA-
 CC A2402 binding CTL, especially having at least 5 amino acids, used for
 CC medicine, particularly anticancer agents, derived from antitumour
 CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 CC genes. The antitumour peptides have cytostatic activities. The peptides
 CC are used for the treatment of cancer. The peptides cause activation of
 CC CTL in cancer patients. The present sequence represents a peptide from
 CC the present invention

XX SQ Sequence 9 AA;

Query Match

Best Local Similarity 53.3%; Score 32; DB 4; Length 9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFHRI 11
 DB 1 KFHRI 6
 |||||

RESULT 6

ABG79075
 ID ABG79075 standard; peptide; 9 AA.

XX AC ABG79075;

XX DT 15-NOV-2002 (first entry)

XX DE Human Cyp-B class I HLA widely expressed antigen peptide #1.

XX KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

XX OS Homo sapiens.

XX XX WO200264057-A2.

XX PD 22-AUG-2002.

XX PF 15-FEB-2002; 2002WO-US005212.

XX PR 15-FEB-2001; 2001US-0268687P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Wang R;

XX DR WPI; 2002-627577/67.

PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.

XX PS Disclosure; Page 17; 61pp; English.

CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention

XX


```

PR 06-OCT-1989; 89JP-00260244.
PR 29-DEC-1989; 89JP-0034705.
PR 19-JUL-1990; 90EP-00307914.
XX
XX (TOFU ) TONEN CORP.
PA
XX
XX Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX
XX WPI; 1995-140755/19.
XX
XX New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
XX the folding of proteins, partic. for activation of inactive recombinant
XX proteins.
XX
XX Example 6; Page 24; 85pp; English.
XX
XX AAR72886-92 are tryptic fragments of E. coli pPase-beta (peptidyl prolyl
XX cis trans isomerase). The E. coli pPase-beta has a single mol. wt. of
XX about 20 kDa and a single isoelectric point of about 5.0. The enzyme
XX catalyses the isomerisation of prolyl peptide bonds in proteins and
XX accelerates the folding of the protein. The inventors are claiming the
XX pPase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated on
XX 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
XX field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 11 AA;
XX
XX Query Match 50.0%; Score 30; DB 2; Length 11;
XX Best Local Similarity 62.5%; Pred.No. 65;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 2 YNNSKFHR 9
XX | : | | |
XX 4 YNNTIFHR 11
XX
XX
XX RESULT 11
XX AAY69962
XX ID AAY69962 standard; peptide; 9 AA.
XX
XX AAY69962;
XX
XX 11-APR-2000 (first entry)
XX
XX Human cyclophilin B peptide fragment #42.
XX
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
XX
XX WO9967288-A1.
XX
XX 29-DEC-1999.
XX
XX 24-JUN-1999; 99WO-JP003360.
XX
XX 25-JUN-1998; 98JP-00178449.
XX
XX (SUMU ) SUMITOMO PHARM CO LTD.
XX (ITOH/) ITOH K.
XX
XX Itoh K, Gomi S;
XX
XX WPI; 2000-116932/10.
XX
XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX diagnosis of tumors.
XX
XX Claim 10; Page 60; 64pp; Japanese.
XX
XX This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B. That

```

CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match 48.3%; Score 29; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPHRVI 11
|:|||||
Db 1 KYHRVI 6

RESULT 12
AAB46946
ID AAB46946 standard; peptide; 9 AA.

XX AAB46946;

DT 04-MAY-2001 (first entry)

XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.

XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW viricide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.

XX Homo sapiens.

XX EP1074267-A1.

XX 07-FEB-2001.

XX 24-JUL-2000; 2000EP-00306263.

XX 22-JUL-1999; 99JP-00207687.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Takasu H, Gotoh M, Yamaoka T;

XX WPI; 2001-193144/20.

XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.

XX Disclosure; Page 19; 25pp; English.

XX This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease

XX Sequence 9 AA;

Query Match 48.3%; Score 29; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPHRVI 11

Db |:|||||
1 KYHRVI 6

RESULT 13

AAB27129
ID AAB27129 standard; protein; 10 AA.

XX AAB27129;

XX 12-FEB-2001 (first entry)

XX Human CASB619 protein epitope SEQ ID NO: 55.

XX Human; CASB619; cancer; autoimmune disease; immunogen; vaccine; epitope.

XX Homo sapiens.

XX WO200058460-A2.

XX 05-OCT-2000.

XX 20-MAR-2000; 2000WO-EP002478.

XX 26-MAR-1999; 99GB-00007113.

XX 25-SEP-1999; 99GB-00022858.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Bruck CEM, Cassart J, Coche T, Vinals Y De BassolsC;

XX WPI; 2000-664923/64.

XX Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT prophylactic and therapeutic treatment of, cancers, particularly ovarian
PT and colon carcinoma, and autoimmune diseases.

XX Example 7; Page 64; 68pp; English.

XX The present sequence comprises an epitope derived from the human CASB619
CC protein sequence. This protein is thought to be specifically or over-
CC expressed in tumour cells, and so can be used as a target for antigen-
CC specific immune responses which can cause destruction of the tumour cell.
CC In addition, the protein and gene can be used in cancer diagnosis, in the
CC treatment of autoimmune diseases and in vaccines against cancer and
CC autoimmune disease. The present sequence can be used as an immunogen

XX Sequence 10 AA;

Query Match 48.3%; Score 29; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKFH 8

Db 1 GYKNNKIH 8

RESULT 14

AAW33943
ID AAW33943 standard; peptide; 9 AA.

XX AAW33943;

XX 28-MAY-1998 (first entry)

XX Betal-adrenergic receptor antagonist.

XX Antagonist; integral membrane protein; inhibitor; transmembrane domain;
KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
KW post-myocardial infarction; HIV infection; cell proliferation disorder;
KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
KW antibacterial; betal-adrenergic receptor.

XX Homo sapiens.
 OS WO9735881-A2.
 PN 02-OCT-1997.
 XX 26-MAR-1997; 97WO-CA000203.
 XX 27-MAR-1996; 96US-0014306P.
 PR 25-JUN-1996; 96US-00670119.
 PR 20-AUG-1996; 96US-0024240P.
 XX (NGGY/) NG G Y K.
 PA (SEEM/) SEEMAN P.
 PA (GEOR/) GEORGE S R.
 PA (ODOW/) O'DOWD B F.
 XX Ng GYK, Seeman P, George SR, Odowd BF;
 XX WPI; 1997-489566/45.
 XX Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Claim 17; Page 94; 127pp; English.
 XX This sequence is a betal-adrenergic receptor antagonist, and is an
 CC antagonist of the invention. The antagonists (A) are for inhibiting the
 CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)
 CC having at least one transmembrane domain (TMD), comprises a peptide
 CC including at least 4 consecutive amino acids (aa) from the sequence of
 CC the TMD. (A) are used to treat or prevent disorders in mammals that
 CC involve disturbances of IMP, and the same effect is achieved by inserting
 CC a nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX Sequence 9 AA;
 SQ Query Match 46.7%; Score 28; DB 2; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYKNSKPH 8
 Db 1 GYANSAPN 8
 RESULT 15
 AAW33942
 ID AAW33942 standard; peptide; 14 AA.
 XX AAW33942;
 XX 28-MAY-1998 (first entry)
 XX Betal-adrenergic receptor antagonist.
 XX Antagonist; integral membrane protein; inhibitor; transmembrane domain;
 KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
 KW

KW post-myocardial infarction; HIV infection; cell proliferation disorder;
 KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
 KW antibacterial; betal-adrenergic receptor.
 XX Homo sapiens.
 OS WO9735881-A2.
 PN 02-OCT-1997.
 XX 26-MAR-1997; 97WO-CA000203.
 XX 27-MAR-1996; 96US-0014306P.
 PR 25-JUN-1996; 96US-00670119.
 PR 20-AUG-1996; 96US-0024240P.
 XX (NGGY/) NG G Y K.
 PA (SEEM/) SEEMAN P.
 PA (GEOR/) GEORGE S R.
 PA (ODOW/) O'DOWD B F.
 XX Ng GYK, Seeman P, George SR, Odowd BF;
 XX WPI; 1997-489566/45.
 XX Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Claim 17; Page 94; 127pp; English.
 XX This sequence is a betal-adrenergic receptor antagonist, and is an
 CC antagonist of the invention. The antagonists (A) are for inhibiting the
 CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)
 CC having at least one transmembrane domain (TMD), comprises a peptide
 CC including at least 4 consecutive amino acids (aa) from the sequence of
 CC the TMD. (A) are used to treat or prevent disorders in mammals that
 CC involve disturbances of IMP, and the same effect is achieved by inserting
 CC a nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX Sequence 14 AA;
 SQ Query Match 46.7%; Score 28; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GYKNSKPH 8
 Db 6 GYANSAPN 13
 RESULT 16
 ABJ15069
 ID ABJ15069 standard; peptide; 14 AA.
 XX ABJ15069;
 XX 10-DEC-2002 (first entry)
 XX Human 125P5C8 epitope #3695.
 DE

XX Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX Homo sapiens.
XX WO200272785-A2.
XX 19-SEP-2002.
XX 13-MAR-2002; 2002WO-US007855.
XX 14-MAR-2001; 2001US-00809638.
XX (AGEN-) AGENSYS INC.
XX Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
DR WPI; 2002-713510/77.
XX New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX Disclosure; Page 216; 274pp; English.
XX The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX Sequence 14 AA;
Query Match 46.7%; Score 28; DB 5; Length 14;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 YKNGKFH 8
Db 4 YENTHFH 10
RESULT 17
ID AAY69959 standard; peptide; 9 AA.
XX AAY69959;
AC AAY69959;
XX 11-APR-2000 (first entry)
DT Human cyclophilin B peptide fragment #39.
DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.
XX WO9967288-A1.
XX 29-DEC-1999.
XX 24-JUN-1999; 99WO-JP003360.
PF 25-JUN-1998; 98JP-00178449.
PR (SUMU) SUMITOMO PHARM CO LTD.
XX (ITO) ITOH K.
XX

PI Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX Claim 4; Page 61; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX Sequence 9 AA;
Query Match 45.0%; Score 27; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 FHRVI 11
Db 2 FHRVI 6
RESULT 18
ID ABR84746 standard; protein; 9 AA.
XX ABR84746;
AC ABR84746;
XX 18-DEC-2003 (first entry)
DT Bovine polypyrimidine tract binding protein conserved nonapeptide.
DE Cow; polypyrimidine tract protein; isoform; RNA stability regulation;
XX immunosuppressive; allograft rejection; CDI54; PTB.
XX Bos taurus.
XX WO2003061581-A2.
XX 31-JUL-2003.
XX 17-JAN-2003; 2003WO-US001623.
XX 17-JAN-2002; 2002US-0349869P.
PR 02-JAN-2003; 2003US-0437779P.
XX (DART-) DARTMOUTH COLLEGE.
XX Rigby WFC;
XX WPI; 2003-778776/73.
XX A new polypyrimidine tract protein isoform useful for finding agents
PT which modulate its activity and to prevent or treat allograft rejection
or CD40 activation.
XX Disclosure; Page 64; 0pp; English.
XX The present invention provides the protein sequence of a polypyrimidine
CC tract protein isoform. Also provided are methods for modulating the
CC stability of a CDI54 RNA. The methods are useful for increasing the
CC stability of a RNA, decreasing the stability of a RNA, preventing or
CC treating allograft rejection in a subject, inhibiting CD40 activation in
CC a subject, and identifying agents that modulate the level or activity of a
CC polypyrimidine tract protein. Agents which modulate the activity of a
CC polypyrimidine tract protein are useful to prevent or treat allograft
CC rejection or inhibit CD40 activation. The present sequence is a
CC nonapeptide conserved between the bovine and human polypyrimidine tract
CC protein
XX

SQ Sequence 9 AA;

Query Match 45.0%; Score 27; DB 7; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKPHR 9
 | | | | |
 Db 2 YGNSPLHR 9

RESULT 19

ADD88599
 ID ADD88599 standard; peptide; 11 AA.

XX

AC ADD88599;

DT 29-JAN-2004 (first entry)

XX

DE Influenza virus H3N2 Replikin #4.

XX

KW vaccine; gene therapy; malaria; influenza; Replikin; haemagglutinin.

XX

OS Orthomyxoviridae.

XX

PN US2003180328-A1.

XX

PD 25-SEP-2003.

XX

PF 26-MAR-2002; 2002US-00105232.

XX

PR 27-MAR-2001; 2001US-0278761P.

XX

PR 09-JUL-2001; 2001US-0303396P.

XX

PR 26-OCT-2001; 2001US-00984057.

XX

PA (BOGO/) BOGOCH S.

XX

PA (BOGO/) BOGOCH E S.

XX

PI Bogoch S, Bogoch ES;

XX

DR WPI; 2003-852213/79.

XX

PT New Replikin peptides of Plasmodium falciparum or influenza virus, useful

XX

PT for diagnosing, preventing or treating influenza virus infection or

XX

PT malaria.

XX

PS Disclosure; SEQ ID NO 266; 136pp; English.

XX

CC The invention relates to an isolated Plasmodium falciparum peptide or an
 CC influenza virus peptide. The composition and methods are useful in
 CC diagnosing, preventing or treating influenza virus infection or malaria.
 CC Also disclosed is an influenza virus vaccine comprising at least one
 CC isolated Replikin present in the haemagglutinin protein of an emerging
 CC strain of influenza virus and a pharmaceutical carrier and/or adjuvant
 CC and a malaria vaccine comprising at least one isolated P. falciparum
 CC Replikin and a pharmaceutical carrier. The present sequence represents
 CC the amino acid sequence of a Replikin sequence.

XX

SQ Sequence 11 AA;

Query Match 45.0%; Score 27; DB 7; Length 11;
 Best Local Similarity 57.1%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSKPHRV 10
 | | | | |
 Db 3 NERFXHI 9

RESULT 20

AAW19409

ID AAW19409 standard; peptide; 11 AA.

XX

AC AAW19409;

XX

DT 04-SEP-1997 (first entry)

XX

DE Anti-fungal and anti-bacterial histatin-based peptide 117.

XX

KW Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

XX

FT Region 1. 11

XX

FT /note= "At least one amino acid must have a D-

XX

FT configuration"

XX

PN WO9640768-A2.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009374.

XX

PR 07-JUN-1995; 95US-00481888.

XX

PA (PERI-) PERIODONTIX INC.

XX

PA (UYBO-) UNIV BOSTON.

XX

PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;

XX

DR WPI; 1997-052232/05.

XX

PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
 PT treating Candidal infections, periodontitis and caries.

XX

PS Claim 2; Fig 1; 72pp; English.

XX

CC The present sequence represents a specifically claimed peptide sequence,
 CC peptide 117, where at least one amino acid is in the D-configuration. The
 CC peptide preferably is modified by an acetyl or carbamyl addition at the N
 CC -terminus and/or amidation at the C-terminus. The peptide, based on the
 CC naturally occurring histidine-rich human histatins, have anti-fungal and
 CC anti-bacterial activity and are useful in compositions for the treatment
 CC of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
 CC ophthalmic fungal or bacterial infections. It is particularly effective
 CC against local and systemic Candida albicans infection, against oral
 CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
 CC Streptococcus mutans and Porphyromonas gingivalis) and against
 CC Clostridium histolyticum. The peptide has superior anti-fungal
 CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
 CC weight basis, compared to the longer, naturally occurring histatins.
 CC Peptides containing D-residues are also more resistant to degradation
 CC than L-amino acid versions

XX

SQ Sequence 11 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
 | | | | |
 Db 5 GYKR-KPH 11

RESULT 21

AAW19455

ID AAW19455 standard; peptide; 11 AA.

XX

AC AAW19455;

XX

```

DT 05-SEP-1997 (first entry)
DE Anti-fungal and anti-bacterial D-amino acid peptide 117.
DE
XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
XX vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1. 11
FT Region
FT /note= "At least one amino acid must have D-
FT configuration"
XX
XX WO9640770-A2.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009962.
XX
XX 07-JUN-1995; 95US-00485273.
XX
XX (PERI-) PERIODONTIX INC.
XX (UYBO-) UNIV BOSTON.
XX
XX Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
XX WPI; 1997-052234/05.
XX
XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
XX peptide(s) - useful esp for treating Candidal infections, periodontitis
XX and caries.
XX
XX Claim 2; Fig 1; 63pp; English.
XX
XX The present sequence represents a specifically claimed example of an anti-
XX fungal and anti-bacterial D-amino acid histatin-based peptide 117, where
XX at least one amino acid in the peptide is in the D-configuration. The
XX peptide is preferably modified by an acetyl or carbamyl addition at the N
XX -terminus and/or amidation at the C-terminus. The novel D-amino acid-
XX containing peptide, based on the naturally occurring histidine-rich human
XX histatins, have anti-fungal and anti-bacterial activity and are useful in
XX compositions for the treatment of oral, vaginal, urethral, mucosal,
XX respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
XX is particularly effective against local and systemic Candida albicans
XX infection, against oral bacterial diseases such as caries and
XX periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
XX gingivalis) and against Clostridium histolyticum. The D-amino acid-
XX containing peptide has superior anti-fungal (especially anti-candidal)
XX and anti-bacterial activity, particularly on a weight basis, compared to
XX the natural L- amino acid forms of histatins and histatin-based peptides.
XX The presence of D-residues also makes the peptides more resistant to
XX degradation than corresponding L-amino acid versions
XX
SQ Sequence 11 AA;
Query Match 44.2%; Score 26.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. NO. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKEH 8
DB 5 GYKR-KFH 11
RESULT 22
AAW19415
ID AAW19415 standard; peptide; 12 AA.
XX
XX AAW19415;
AC

```

```

XX 05-SEP-1997 (first entry)
XX
XX Anti-fungal and anti-bacterial histatin-based peptide 113-P5.
XX
XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
XX vaginal infection; urethral infection; mucosal infection; ear infection;
KW respiratory infection; skin infection; ophthalmic infection;
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
KW Clostridium histolyticum.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1. 12
FT Region
FT /note= "At least one amino acid must have a D-
FT configuration"
XX
XX WO9640768-A2.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009374.
XX
XX 07-JUN-1995; 95US-00481888.
XX
XX (PERI-) PERIODONTIX INC.
XX (UYBO-) UNIV BOSTON.
XX
XX Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX WPI; 1997-052232/05.
XX
XX Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
XX treating Candidal infections, periodontitis and caries.
XX
XX Claim 2; Fig 1; 72pp; English.
XX
XX The present sequence represents a specifically claimed peptide sequence,
XX peptide 113-P5, where at least one amino acid is in the D-configuration.
XX The peptide preferably is modified by an acetyl or carbamyl addition at
XX the N-terminus and/or amidation at the C-terminus. The peptide, based on
XX the naturally occurring histidine-rich human histatins, have anti- fungal
XX and anti-bacterial activity and are useful in compositions for the
XX treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
XX ophthalmic fungal or bacterial infections. It is particularly effective
XX against local and systemic Candida albicans infection, against oral
XX bacterial diseases such as caries and periodontitis (by inhibiting e.g.
XX Streptococcus mutans and Porphyromonas gingivalis) and against
XX Clostridium histolyticum. The peptide has superior anti-fungal
XX (especially anti-Candidal) and anti-bacterial activity, particularly on a
XX weight basis, compared to the longer, naturally occurring histatins.
XX Peptides containing D-residues are also more resistant to degradation
XX than L-amino acid versions
XX
SQ Sequence 12 AA;
Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKEH 8
DB 6 GYKR-KFH 12
RESULT 23
AAW19417
ID AAW19417 standard; peptide; 12 AA.
XX
XX AAW19417;
AC
XX 05-SEP-1997 (first entry)

```

XX DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.5.
XX DE
XX KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
XX KW vaginal infection; urethral infection; mucosal infection; ear infection;
XX KW respiratory infection; skin infection; ophthalmic infection;
XX KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
XX KW Clostridium histolyticum.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Region 1. .12
XX FT /note= "At least one amino acid must have a D-
XX FT configuration"
XX FT
XX PN WO9640768-A2.
XX XX
XX XX 19-DEC-1996.
XX XX
XX XX 07-JUN-1996; 96WO-US009374.
XX XX
XX XX 07-JUN-1995; 95US-00481888.
XX XX
XX XX (PERI-) PERIODONTIX INC.
XX XX (UYBO-) UNIV BOSTON.
XX PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX DR WPI; 1997-052232/05.
XX XX
XX PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
XX PT treating Candidal infections, peridontitis and caries.
XX XX
XX PS Claim 2; Fig 1; 72pp; English.
XX XX
XX CC The present sequence represents a specifically claimed peptide sequence,
XX CC peptide 113-F4.5, where at least one amino acid is in the D-
XX CC configuration. The peptide preferably is modified by an acetyl or
XX CC carbamyl addition at the N-terminus and/or amidation at the C-terminus.
XX CC The peptide, based on the naturally occurring histidine-rich human
XX CC histatins, have anti-fungal and anti-bacterial activity and are useful in
XX CC compositions for the treatment of oral, vaginal, urethral, mucosal,
XX CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
XX CC is particularly effective against local and systemic Candida albicans
XX CC infection, against oral bacterial diseases such as caries and
XX CC peridontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
XX CC gingivalis) and against Clostridium histolyticum. The peptide has
XX CC superior anti-fungal (especially anti-Candidal) and anti-bacterial
XX CC activity, particularly on a weight basis, compared to the longer,
XX CC naturally occurring histatins. Peptides containing D-residues are also
XX CC more resistant to degradation than L-amino acid versions
XX XX
XX SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 24
AAW19414
ID AAW19414 standard; peptide; 12 AA.
XX
XX AC AAW19414;
XX
XX DT 05-SEP-1997 (first entry)
XX
XX DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.

XX KW Candida albicans; peridontitis; caries; tooth decay; oral infection;
XX KW vaginal infection; urethral infection; mucosal infection; ear infection;
XX KW respiratory infection; skin infection; ophthalmic infection;
XX KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
XX KW Clostridium histolyticum.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Region 1. .12
XX FT /note= "At least one amino acid must have a D-
XX FT configuration"
XX FT
XX PN WO9640768-A2.
XX XX
XX XX 19-DEC-1996.
XX XX
XX XX 07-JUN-1996; 96WO-US009374.
XX XX
XX XX 07-JUN-1995; 95US-00481888.
XX XX
XX XX (PERI-) PERIODONTIX INC.
XX XX (UYBO-) UNIV BOSTON.
XX PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
XX DR WPI; 1997-052232/05.
XX XX
XX PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
XX PT treating Candidal infections, peridontitis and caries.
XX XX
XX PS Claim 2; Fig 1; 72pp; English.
XX XX
XX CC The present sequence represents a specifically claimed peptide sequence,
XX CC peptide 113-F4, where at least one amino acid is in the D-configuration.
XX CC The peptide preferably is modified by an acetyl or carbamyl addition at
XX CC the N-terminus and/or amidation at the C-terminus. The peptide, based on
XX CC the naturally occurring histidine-rich human histatins, have anti-
XX CC fungal and anti-bacterial activity and are useful in compositions for the
XX CC treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
XX CC ophthalmic fungal or bacterial infections. It is particularly effective
XX CC against local and systemic Candida albicans infection, against oral
XX CC bacterial diseases such as caries and peridontitis (by inhibiting e.g.
XX CC Streptococcus mutans and Porphyromonas gingivalis) and against
XX CC Clostridium histolyticum. The peptide has superior anti-fungal
XX CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
XX CC weight basis, compared to the longer, naturally occurring histatins.
XX CC Peptides containing D-residues are also more resistant to degradation
XX CC than L-amino acid versions
XX XX
XX SQ Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 25
AAW19407
ID AAW19407 standard; peptide; 12 AA.
XX
XX AC AAW19407;
XX
XX DT 04-SEP-1997 (first entry)
XX
XX DE Anti-fungal and anti-bacterial histatin-based peptide 113.
XX
XX KW Candida albicans; peridontitis; caries; tooth decay; oral infection;

XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Region 1. .12
 FT /note= "At least one amino acid must have D-configuration"
 XX WO9640770-A2.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US009962.
 XX 07-JUN-1995; 95US-00485273.
 XX (PERI-) PERIODONTIX INC.
 XX (UYBO-) UNIV BOSTON.
 XX Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
 XX WPI; 1997-052234/05.
 XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based peptide(s) - useful esp for treating Candidal infections, periodontitis and caries.
 XX Claim 2; Fig 1; 63pp; English.
 XX The present sequence represents a specifically claimed example of an anti-fungal and anti-bacterial D-amino acid histatin-based peptide 113, where at least one amino acid in the peptide is in the D-configuration. The peptide is preferably modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The novel D-amino acid-containing peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against Clostridium histolyticum. The D-amino acid-containing peptide has superior anti-fungal (especially anti-candidal) and anti-bacterial activity, particularly on a weight basis, compared to the natural L- amino acid forms of histatins and histatin-based peptides. The presence of D-residues also makes the peptides more resistant to degradation than corresponding L-amino acid versions

XX SQ Sequence 12 AA;
 Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKPF 8
 ||| |||
 Db 6 GYKR-KFH 12

RESULT 28
 AAW19461
 ID AAW19461 standard; peptide; 12 AA.
 XX AAW19461;
 XX 05-SEP-1997 (first entry)
 XX Anti-fungal and anti-bacterial D-amino acid peptide 113-F5.
 XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;

KW Clostridium histolyticum.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Region 1. .12
 FT /note= "At least one amino acid must have D-configuration"
 XX WO9640770-A2.
 XX 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US009962.
 XX 07-JUN-1995; 95US-00485273.
 XX (PERI-) PERIODONTIX INC.
 XX (UYBO-) UNIV BOSTON.
 XX Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
 XX WPI; 1997-052234/05.
 XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based peptide(s) - useful esp for treating Candidal infections, periodontitis and caries.
 XX Claim 2; Fig 1; 63pp; English.
 XX The present sequence represents a specifically claimed example of an anti-fungal and anti-bacterial D-amino acid histatin-based peptide 113-F5, where at least one amino acid in the peptide is in the D-configuration. The peptide is preferably modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The novel D-amino acid-containing peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against oral bacterial diseases such as Porphyromonas gingivalis) and against Clostridium histolyticum. The D-amino acid-containing peptide has superior anti-fungal (especially anti-candidal) and anti-bacterial activity, particularly on a weight basis, compared to the natural L- amino acid forms of histatins and histatin-based peptides. The presence of D-residues also makes the peptides more resistant to degradation than corresponding L-amino acid versions

XX SQ Sequence 12 AA;
 Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKPF 8
 ||| |||
 Db 6 GYKR-KFH 12

RESULT 29
 AAW19460
 ID AAW19460 standard; peptide; 12 AA.
 XX AAW19460;
 XX 05-SEP-1997 (first entry)
 XX Anti-fungal and anti-bacterial D-amino acid peptide 113-F4.
 XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;

KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum.

OS Synthetic.

XX Key Location/Qualifiers
 XX Region 1..12
 FT /note= "At least one amino acid must have D-
 FT configuration"

XX WO9640770-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009962.

XX 07-JUN-1995; 95US-00485273.

XX (PERI-) PERIODONTIX INC.

XX (UYBO-) UNIV BOSTON.

XX Oppenheim FG, Xu T, Spacciapoli P, Roberts PD, Friden PM;

XX WPI; 1997-052234/05.

XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 XX peptide(s) - useful esp for treating Candidal infections, periodontitis
 XX and caries.

XX Claim 2; Fig 1; 63pp; English.

XX The present sequence represents a specifically claimed example of an anti-
 CC fungal and anti-bacterial D-amino acid histatin-based peptide 113-P4,
 CC where at least one amino acid in the peptide is in the D-configuration.
 CC The peptide is preferably modified by an acetyl or carbamyl addition at
 CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
 CC -containing peptide, based on the naturally occurring histidine-rich
 CC human histatins, have anti-fungal and anti-bacterial activity and are
 CC useful in compositions for the treatment of oral, vaginal, urethral,
 CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
 CC infections. It is particularly effective against local and systemic
 CC Candida albicans infection, against oral bacterial diseases such as
 CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
 CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
 CC amino acid-containing peptide has superior anti-fungal (especially anti-
 CC candidal) and anti-bacterial activity, particularly on a weight basis,
 CC compared to the natural L- amino acid forms of histatins and histatin-
 CC based peptides. The presence of D-residues also makes the peptides more
 CC resistant to degradation than corresponding L-amino acid versions

XX Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
 |||||
 DB 6 GYKR-KFH 12

RESULT 30

AAWI9463

ID AAWI9463 standard; peptide; 12 AA.

XX AAWI9463;

XX 05-SEP-1997 (first entry)

XX Anti-fungal and anti-bacterial D-amino acid peptide 113-P4.5.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KW vaginal infection; urethral infection; mucosal infection; ear infection;

KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum.

OS Synthetic.

XX Key Location/Qualifiers
 XX Region 1..12
 FT /note= "At least one amino acid must have D-
 FT configuration"

XX WO9640770-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009962.

XX 07-JUN-1995; 95US-00485273.

XX (PERI-) PERIODONTIX INC.

XX (UYBO-) UNIV BOSTON.

XX Oppenheim FG, Xu T, Spacciapoli P, Roberts PD, Friden PM;

XX WPI; 1997-052234/05.

XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 XX peptide(s) - useful esp for treating Candidal infections, periodontitis
 XX and caries.

XX Claim 2; Fig 1; 63pp; English.

XX The present sequence represents a specifically claimed example of an anti-
 CC fungal and anti-bacterial D-amino acid histatin-based peptide 113-P4.5,
 CC where at least one amino acid in the peptide is in the D-configuration.
 CC The peptide is preferably modified by an acetyl or carbamyl addition at
 CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
 CC -containing peptide, based on the naturally occurring histidine-rich
 CC human histatins, have anti-fungal and anti-bacterial activity and are
 CC useful in compositions for the treatment of oral, vaginal, urethral,
 CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
 CC infections. It is particularly effective against local and systemic
 CC Candida albicans infection, against oral bacterial diseases such as
 CC caries and periodontitis (by inhibiting e.g. Streptococcus mutans and
 CC Porphyromonas gingivalis) and against Clostridium histolyticum. The D-
 CC amino acid-containing peptide has superior anti-fungal (especially anti-
 CC candidal) and anti-bacterial activity, particularly on a weight basis,
 CC compared to the natural L- amino acid forms of histatins and histatin-
 CC based peptides. The presence of D-residues also makes the peptides more
 CC resistant to degradation than corresponding L-amino acid versions

XX Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8
 |||||
 DB 6 GYKR-KFH 12

RESULT 31

AAWI9472

ID AAWI9472 standard; peptide; 12 AA.

XX AAWI9472;

XX 05-SEP-1997 (first entry)

XX Anti-fungal and anti-bacterial D-amino acid peptide 113-Q3.9.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;

KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum.

XX Synthetic.

XX Key Location/Qualifiers
 PH Region 1. 12

FT /note= "At least one amino acid must have D-
 FT configuration"

XX WO9640770-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009962.

XX 07-JUN-1995; 95US-00485273.

XX (PERI-) PERIODONTIX INC.
 XX (UYBO-) UNIV BOSTON.

XX Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;
 PI WPI; 1997-052234/05.

XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 PT peptides(s) - useful esp for treating Candidal infections, periodontitis
 PT and caries.

XX Claim 2; Fig 1; 63pp; English.

XX The present sequence represents a specifically claimed example of an anti-
 CC -fungal and anti-bacterial D-amino acid histatin-based peptide 113-Q3.9,
 CC where at least one amino acid in the peptide is in the D-configuration.
 CC The peptide is preferably modified by an acetyl or carbamyl addition at
 CC the N-terminus and/or amidation at the C-terminus. The novel D-amino acid
 CC -containing peptide, based on the naturally occurring histidine-rich
 CC human histatins, have anti-fungal and anti-bacterial activity and are
 CC useful in compositions for the treatment of oral, vaginal, urethral,
 CC mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial
 CC infections. It is particularly effective against local and systemic
 CC Candida albicans infection, against e.g. Streptococcus mutans and
 CC Porphyromonas gingivalis (by inhibiting e.g. Streptococcus mutans and
 CC amino acid-containing peptide has superior anti-fungal (especially anti-
 CC candidal) and anti-bacterial activity, particularly on a weight basis,
 CC compared to the natural L- amino acid forms of histatins and histatin-
 CC based peptides. The presence of D-residues also makes the peptides more
 CC resistant to degradation than corresponding L-amino acid versions

XX Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
 ||| |||
 Db 6 GYK-QKPH 12

RESULT 32

AAV25141
 ID AAY25141 standard; peptide; 12 AA.

XX AAY25141;

XX 27-AUG-1999 (first entry)

XX Antibacterial and antifungal peptide 2.

KW Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;
 KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
 XX Unidentified.

XX WO9931123-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-US026513.

XX 18-DEC-1997; 97US-00993235.

XX (PERI-) PERIODONTIX INC.
 XX (UYBO-) UNIV BOSTON.

XX Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
 XX WPI; 1999-395161/33.

XX Antibacterial and antifungal peptides.

XX Disclosure; Page 7; 31pp; English.

XX This invention describes novel substantially pure antibacterial and
 CC antifungal peptides (A) containing between 13 and 20 amino acids, where
 CC the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10-
 CC R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or
 CC absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or
 CC absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another
 CC basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another
 CC hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent;
 CC R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where
 CC Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the
 CC amino acid sequence. (A) can be used to treat fungal or bacterial
 CC infection in a mammal. The peptides are particularly used to treat
 CC candidal infection, as well as bacterial and viral infections, especially
 CC vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic
 CC infections. The infections that can be treated include those caused by
 CC Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces
 CC viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes
 CC ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter
 CC showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga
 CC ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella
 CC corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium
 CC periodonticum, Peptostreptococcus nicos, Porphyromonas endodontalis,
 CC Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens,
 CC Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by
 CC various Staphylococcal and Streptococcal species. AAY25140-Y25149 are
 CC peptides used in the description of the invention

XX Sequence 12 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
 ||| |||
 Db 6 GYKR-KPH 12

RESULT 33

AAV25143
 ID AAY25143 standard; peptide; 12 AA.

XX AAY25143;

XX 27-AUG-1999 (first entry)

XX Antibacterial and antifungal peptide 4.

XX Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;

KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
XX Unidentified.
OS WO9931123-A1.
PN 24-JUN-1999.
XX 14-DEC-1998; 98WO-US026513.
XX 18-DEC-1997; 97US-00993235.
XX (PERI-) PERIODONTIX INC.
XX (UYBO-) UNIV BOSTON.
PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
XX WPI; 1999-395161/33.
DR Antibacterial and antifungal peptides.
XX Disclosure; Page 7; 31pp; English.
XX This invention describes novel substantially pure antibacterial and antifungal peptides (A) containing between 13 and 20 amino acids, where the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10- R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent; R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the amino acid sequence. (A) can be used to treat fungal or bacterial infection in a mammal. The peptides are particularly used to treat candidal infection, as well as bacterial and viral infections, especially vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic infections. The infections that can be treated include those caused by Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium periodonticum, Peptostreptococcus nicotus, Porphyromonas endodontalis, Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens, Porphyromonas acnes, Pseudomonas aeruginosa, and those caused by Propionibacterium acnes, Streptococcus species. AAY25140-Y25149 are various Staphylococcal and Streptococcal species. AAY25140-Y25149 are peptides used in the description of the invention

XX SQ Sequence 12 AA;
Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKPH 8
||| |||
Db 6 GYKR-KPH 12

RESULT 34
AAY25140
ID AAY25140 standard; peptide; 12 AA.
XX AAY25140;
XX 27-AUG-1999 (first entry)
DT Antibacterial and antifungal peptide 1.
DE Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;
XX viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.
KW

XX Unidentified.
XX WO9931123-A1.
PN 24-JUN-1999.
XX 14-DEC-1998; 98WO-US026513.
XX 18-DEC-1997; 97US-00993235.
XX (PERI-) PERIODONTIX INC.
XX (UYBO-) UNIV BOSTON.
PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;
XX WPI; 1999-395161/33.
DR Antibacterial and antifungal peptides.
XX Disclosure; Page 7; 31pp; English.
XX This invention describes novel substantially pure antibacterial and antifungal peptides (A) containing between 13 and 20 amino acids, where the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8- R9-R10- R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or absent; R4 is Ala; R5, R6, R9, R12, R13, are Lys, Gln, Arg or another basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent; R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the amino acid sequence. (A) can be used to treat fungal or bacterial infection in a mammal. The peptides are particularly used to treat candidal infection, as well as bacterial and viral infections, especially vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic infections. The infections that can be treated include those caused by Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces viscosus, Bacteriodes forsythus, Bacteriodes gracilis, Bacteriodes ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Eikenella corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium periodonticum, Peptostreptococcus nicotus, Porphyromonas endodontalis, Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens, Porphyromonas acnes, Pseudomonas aeruginosa, and those caused by Propionibacterium acnes, Streptococcus species. AAY25140-Y25149 are various Staphylococcal and Streptococcal species. AAY25140-Y25149 are peptides used in the description of the invention

XX SQ Sequence 12 AA;
Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKPH 8
||| |||
Db 6 GYKR-KPH 12

RESULT 35
AAB11990
ID AAB11990 standard; peptide; 12 AA.
XX AAB11990;
XX 24-NOV-2000 (first entry)
DT Histatin-related peptide, P-113-R3.9K.
DE Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
XX antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
KW
XX

OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 12
 FT /note= "C-terminal amide"
 XX
 XX W0200040204-A2.
 XX
 XX 13-JUL-2000.
 XX
 XX 07-JAN-2000; 2000WO-US000480.
 XX
 XX 08-JAN-1999; 99US-00226666.
 XX (PERI-) PERIODONTIX INC.
 XX
 XX Spacciapoli P, Rothstein DM, Friden PM;
 XX WPI; 2000-465852/40.
 XX
 XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
 PT infections in a mammal comprises administering histatin or a fragment of
 PT it.
 XX
 XX Example 6; Page 13; 27pp; English.
 XX
 CC The invention relates to treating cystic fibrosis via the administration
 CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
 CC peptide that is administered contains between 8 and 20 amino acids and
 CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
 CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
 CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
 CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
 CC another basic amino acid; X7 is His, Phe, Tyr, Leu, or another hydrophobic
 CC amino acid; X8 is His, Phe, Tyr, Leu, or another hydrophobic amino acid;
 CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
 CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
 CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
 CC basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr,
 CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
 CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
 CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
 CC absent. Optionally, the peptide may contain at least one modification
 CC selected from an N-terminal acyl addition, an N-terminal carbamyl
 CC addition and a C-terminal amide addition. Histatin, histatin fragments
 CC and histatin-related peptides have activity against Pseudomonas
 CC aeruginosa. They may therefore be used to combat Pseudomonas
 CC and other pulmonary infections in cystic fibrosis patients. Such
 CC infections are often resistant to the antibiotics normally used to treat
 CC pulmonary infections. Sequences AAB11976-B11993 represent histatin-
 CC related peptides used in the exemplifications of the invention. With the
 CC exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
 CC activity against Pseudomonas aeruginosa
 XX
 XX Sequence 12 AA;
 XX
 Query Match 44.2%; Score 26.5; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKPH 8
 ||| |||
 Db 6 GYK-KKPH 12
 RESULT 36
 AAB11976
 ID AAB11976 standard; peptide; 12 AA.
 XX
 AC AAB11976;
 XX
 XX 24-NOV-2000 (first entry)

XX Histatin-related peptide, P-113.
 DE
 XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
 KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
 KW
 XX Homo sapiens.
 OS
 XX W0200040204-A2.
 FN
 XX 13-JUL-2000.
 PD
 XX 07-JAN-2000; 2000WO-US000480.
 PF
 XX 08-JAN-1999; 99US-00226666.
 XX (PERI-) PERIODONTIX INC.
 XX
 XX Spacciapoli P, Rothstein DM, Friden PM;
 PI
 XX WPI; 2000-465852/40.
 DR
 XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
 PT infections in a mammal comprises administering histatin or a fragment of
 PT it.
 PT
 XX
 XX Claim 4; Page 16; 27pp; English.
 PS
 XX The invention relates to treating cystic fibrosis via the administration
 CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
 CC peptide that is administered contains between 8 and 20 amino acids and
 CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
 CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
 CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
 CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
 CC another basic amino acid; X7 is His, Phe, Tyr, Leu, or another hydrophobic
 CC amino acid; X8 is His, Phe, Tyr, Leu, or another hydrophobic amino acid;
 CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
 CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
 CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
 CC basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr,
 CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
 CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
 CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
 CC absent. Optionally, the peptide may contain at least one modification
 CC selected from an N-terminal acyl addition, an N-terminal carbamyl
 CC addition and a C-terminal amide addition. Histatin, histatin fragments
 CC and histatin-related peptides have activity against Pseudomonas
 CC aeruginosa. They may therefore be used to combat Pseudomonas
 CC and other pulmonary infections in cystic fibrosis patients. Such
 CC infections are often resistant to the antibiotics normally used to treat
 CC pulmonary infections. Sequences AAB11976-B11984 represent specifically
 CC claimed histatin-related peptides for use in the method of the invention.
 CC The present sequence corresponds to residues 4-15 of naturally-occurring
 CC human histatin 3 and histatin 5 (AAB11974, AAB11975)
 XX
 XX Sequence 12 AA;
 XX
 Query Match 44.2%; Score 26.5; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKPH 8
 ||| |||
 Db 6 GYK-KKPH 12
 RESULT 37
 AAB11985
 ID AAB11985 standard; peptide; 12 AA.
 XX
 AC AAB11985;
 XX

DT 24-NOV-2000 (first entry)
XX Histatin-related peptide, P-113-NA.
XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
XX antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 12 /note= "C-terminal amide"
FT
XX WO200040204-A2.
XX 13-JUL-2000.
XX 07-JAN-2000; 2000WO-US000480.
XX 08-JAN-1999; 99US-00226666.
XX (PERI-) PERIODONTIX INC.
XX Spacciapoli P, Rothstein DM, Friden PM;
XX WPI; 2000-465852/40.
XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
XX infections in a mammal comprises administering histatin or a fragment of
XX it.
XX Example 4; Page 12; 27pp; English.
XX The invention relates to treating cystic fibrosis via the administration
XX of a histatin, a fragment of histatin, or a histatin-related peptide. The
XX peptide that is administered contains between 8 and 20 amino acids and
XX has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
XX X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
XX Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
XX another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
XX amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
XX X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
XX His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
XX Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
XX basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
XX Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
XX is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
XX or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
XX absent. Optionally, the peptide may contain at least one modification
XX selected from an N-terminal acyl addition, an N-terminal carbamyl
XX addition and a C-terminal amide addition. Histatin, histatin fragments
XX and histatin-related peptides have activity against Pseudomonas
XX aeruginosa. They may therefore be used to combat Pseudomonas infections
XX and other pulmonary infections in cystic fibrosis patients. Such
XX infections are often resistant to the antibiotics normally used to treat
XX pulmonary infections. Sequences AAB11985-B11993 represent histatin-
XX related peptides used in the exemplifications of the invention. With the
XX exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
XX activity against Pseudomonas aeruginosa
XX Sequence 12 AA;
XX Query Match 44.2%; Score 26.5; DB 3; Length 12;
XX Best Local Similarity 75.0%; Pred. No. 3.3e+02;
XX Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX 1 GYKSKFPH 8
XX |||||
XX 6 GYKR-KFH 12

RESULT 38
AAB11987
ID AAB11987 standard; peptide; 12 AA.
XX AAB11987;
XX 24-NOV-2000 (first entry)
XX Histatin-related peptide, P-113-Q3.9.
XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
XX antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX Modified-site 12 /note= "C-terminal amide"
FT
XX WO200040204-A2.
XX 13-JUL-2000.
XX 07-JAN-2000; 2000WO-US000480.
XX 08-JAN-1999; 99US-00226666.
XX (PERI-) PERIODONTIX INC.
XX Spacciapoli P, Rothstein DM, Friden PM;
XX WPI; 2000-465852/40.
XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
XX infections in a mammal comprises administering histatin or a fragment of
XX it.
XX Example 5; Page 12; 27pp; English.
XX The invention relates to treating cystic fibrosis via the administration
XX of a histatin, a fragment of histatin, or a histatin-related peptide. The
XX peptide that is administered contains between 8 and 20 amino acids and
XX has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
XX X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
XX Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
XX another basic amino acid; X7 is His, Phe, Tyr Leu, or another hydrophobic
XX amino acid; X8 is His, Phe, Tyr Leu, or another hydrophobic amino acid;
XX X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
XX His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
XX Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
XX basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
XX Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
XX is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
XX or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
XX absent. Optionally, the peptide may contain at least one modification
XX selected from an N-terminal acyl addition, an N-terminal carbamyl
XX addition and a C-terminal amide addition. Histatin, histatin fragments
XX and histatin-related peptides have activity against Pseudomonas
XX aeruginosa. They may therefore be used to combat Pseudomonas infections
XX and other pulmonary infections in cystic fibrosis patients. Such
XX infections are often resistant to the antibiotics normally used to treat
XX pulmonary infections. Sequences AAB11985-B11993 represent histatin-
XX related peptides used in the exemplifications of the invention. With the
XX exception of P-113-Q2.3.9.10 (AAB11988), all these peptides showed
XX activity against Pseudomonas aeruginosa
XX Sequence 12 AA;
XX Query Match 44.2%; Score 26.5; DB 3; Length 12;
XX Best Local Similarity 75.0%; Pred. No. 3.3e+02;
XX Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX 1 GYKSKFPH 8
XX |||||
XX 6 GYKR-KFH 12

Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKPH 8
Db 6 GYK-QKPH 12
RESULT 39
AAB11977
ID AAB11977 standard; peptide; 12 AA.
AC AAB11977;
XX 24-NOV-2000 (first entry)
XX Histatin-related peptide, P-113 (D-form).
XX Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;
KW antibiotic resistance; pulmonary infection; antibacterial; antibiotic.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 1. .12
FT /note= "All D-form residues"
XX WO2000040204-A2.
XX 13-JUL-2000.
XX 07-JAN-2000; 2000WO-US000480.
XX 08-JAN-1999; 99US-00226666.
XX (PERI-) PERIODONTIX INC.
XX Spacciapoli P, Rothstein DM, Friden PM;
XX WPI; 2000-465852/40.
XX Treating cystic fibrosis and combating Pseudomonas and other pulmonary
PT infections in a mammal comprises administering histatin or a fragment of
PT it.
XX Claim 5; Page 16; 27pp; English.
CC The invention relates to treating cystic fibrosis via the administration
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The
CC peptide that is administered contains between 8 and 20 amino acids and
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-
CC X17-X18-X19-X20- X21-X22-X23 where X1 is Asp or absent; X2 is Ser or
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or
CC another basic amino acid; X7 is His, Phe, Tyr, Leu, or another hydrophobic
CC amino acid; X8 is His, Phe, Tyr, Leu, or another hydrophobic amino acid;
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another
CC basic amino acid, or absent; X14 is Phe or absent X15 is His, Phe, Tyr,
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or
CC absent. Optionally, the peptide may contain at least one modification
CC selected from an N-terminal acyl addition, an N-terminal carbamyl
CC addition and a C-terminal amide addition. Histatin, histatin fragments
CC and histatin-related peptides have activity against Pseudomonas
CC aeruginosa. They may therefore be used to combat Pseudomonas infections
CC and other pulmonary infections in cystic fibrosis patients. Such
CC infections are often resistant to the antibiotics normally used to treat
CC pulmonary infections. Sequences AAB11976-B11984 represent specifically
CC claimed histatin-related peptides for use in the method of the invention

XX SQ Sequence 12 AA;
Query Match 44.2%; Score 26.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKPH 8
Db 6 GYKR-KFH 12
RESULT 40
ADB81288
ID ADB81288 standard; peptide; 12 AA.
XX AC ADB81288;
XX 04-DEC-2003 (first entry)
XX Biologically active histatin peptide (SeqID 22).
XX peptide synthesis; protegrin IB-367; hybrid process; microflora;
KW antibacterial; oral mucositis; histatin.
XX Synthetic.
XX WO2003062266-A2.
XX 31-JUL-2003.
XX 22-JAN-2003; 2003WO-US001998.
XX 22-JAN-2002; 2002US-0350449P.
XX (INTR-) INTRABIOTICS PHARM INC.
XX Merutka G, Zhu Z, Almeda SA;
XX WPI; 2003-663393/62.
XX Synthesizing protegrin IB-367 peptide used for treating infectious
PT diseases, by solid phase synthesis of specific side chain protected
PT peptide, using side chain non-protected arginine reagents and
PT deprotecting side chain protected peptide.
XX Disclosure; Page 8; 70pp; English.
XX This invention relates to a novel method for peptide synthesis.
CC Specifically, it refers to the synthesis of the protegrin IB-367 peptide
CC by a hybrid process, which comprises carrying out both solid phase
CC synthesis as well as liquid phase synthesis methods. The present
CC invention describes synthesizing specific side chain protected peptide
CC fragment intermediates using non-protected arginine reagents, and
CC deprotecting the side chain protected peptide. The protegrin IB-367
CC peptide is active in vitro and in vivo against microflora, such that it
CC is described as having antibacterial properties and can be used for
CC treating oral mucositis. Furthermore it is useful for coupling to
CC therapeutic agents, reporter molecules, diagnostic agents and antibody
CC molecules. This peptide sequence is the histatin peptide (SeqID 22),
CC synthesised by the method of the invention.
XX SQ Sequence 12 AA;
Query Match 44.2%; Score 26.5; DB 7; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GYKNSKPH 8
Db 6 GYKR-KFH 12

RESULT 41
 AAR89887
 ID AAR89887 standard; peptide; 14 AA.
 XX
 AC AAR89887;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-JUL-1996 (first entry)
 XX
 DE Human histatin 3 fragment, 3P4.
 XX
 KW Histidine-rich salivary protein; HRP; human; macaque; histatin 1;
 KW histatin 3; Candida albicans; blastoconidia; inhibition; C. albicans;
 KW parotid salivary secretion.
 XX
 OS Homo sapiens.
 XX
 PN US5486503-A.
 XX
 PD 23-JAN-1996.
 XX
 PF 09-AUG-1994; 94US-00287717.
 XX
 PR 01-NOV-1991; 91US-00786571.
 PR 28-OCT-1993; 93US-00145030.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Xu T, Oppenheim FG;
 XX
 DR WPI; 1996-097084/10.
 XX
 PT Treatment of fungal infection with histatins or derived peptide(s) -
 PT mostly new cpds., partic. for treating or preventing infection by Candida
 PT albicans.
 XX
 PS Claim 3; Fig 1; 19pp; English.
 XX
 CC The sequences given in AAR89883-92 are peptide fragments derived from the
 CC histidine-rich salivary protein, human and macaque histatin 1 and
 CC histatin 3. This sequence represents residues 9-22 of human histatin 3.
 CC These peptides are used to treat or prevent infection by Candida albicans
 CC in human or veterinary medicine. These peptides are more active than
 CC native histatins. These peptides were tested in three assays designed to
 CC measure separately their effectiveness in killing of blastoconidia, in
 CC killing of germinated cells, and in inhibiting the germination of C.
 CC albicans. For these assays, human histatin 3 was isolated from human
 CC parotid salivary secretions, and macaque histatin 1 was chemically
 CC synthesised. Compositions containing these peptides may also be used in
 CC the treatment of bacterial infections, e.g. Streptococcus mutans or P.
 CC gingivalis, or viral infections, e.g. Herpes simplex or HIV-1. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 14 AA;
 Query Match 44.2%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKFH 8
 ||| |||
 Db 1 GYKR-KFH 7
 RESULT 42
 AAW19441
 ID AAW19441 standard; peptide; 14 AA.
 XX
 AC AAW19441;
 XX
 DT 05-SEP-1997 (first entry)
 DT
 XX
 DE Anti-fungal and anti-bacterial histatin-based histatin 104.

XX
 KW Candida albicans; periodontitis; caries; tooth decay; oral infection;
 KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1.14
 FT /note= "At least one amino acid must have a D-
 FT configuration"
 XX
 PN W09640768-A2.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009374.
 XX
 PR 07-JUN-1995; 95US-00481888.
 XX
 PA (PERI-) PERIODONTIX INC.
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;
 XX
 DR WPI; 1997-052232/05.
 XX
 PT Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for
 PT treating Candidal infections, periodontitis and caries.
 XX
 PS Disclosure; Fig 1; 72pp; English.
 XX
 CC The present sequence represents histatin 104, found in human paratoid
 CC secretion, where at least one amino acid is in the D-configuration. The
 CC peptide preferably is modified by an acetyl or carbamyl addition at the N
 CC terminus and/or amidation at the C-terminus. The peptide, based on the
 CC naturally occurring histidine-rich human histatins, have anti-fungal and
 CC anti-bacterial activity and are useful in compositions for the treatment
 CC of oral, vaginal, urethral, mucosal, respiratory, skin, ear and
 CC ophthalmic fungal or bacterial infections. It is particularly effective
 CC against local and systemic Candida albicans infection, against oral
 CC bacterial diseases such as caries and periodontitis (by inhibiting e.g.
 CC Streptococcus mutans and Porphyromonas gingivalis) and against
 CC Clostridium histolyticum. The peptide has superior anti-fungal
 CC (especially anti-Candidal) and anti-bacterial activity, particularly on a
 CC weight basis, compared to the longer, naturally occurring histatins.
 CC Peptides containing D-residues are also more resistant to degradation
 CC than L-amino acid versions
 XX
 SQ Sequence 14 AA;
 Query Match 44.2%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GYKNSKFH 8
 ||| |||
 Db 1 GYKR-KFH 7
 RESULT 43
 AAW19452
 ID AAW19452 standard; peptide; 14 AA.
 XX
 AC AAW19452;
 XX
 DT 05-SEP-1997 (first entry)
 DT
 XX
 DE Anti-fungal and anti-bacterial D-amino acid peptide 104.
 XX
 KW Candida albicans; periodontitis; caries; tooth decay; oral infection;

KW vaginal infection; urethral infection; mucosal infection; ear infection;
 KW respiratory infection; skin infection; ophthalmic infection;
 KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;
 KW Clostridium histolyticum.

XX Synthetic.

XX Key Location/Qualifiers
 FH Region 1..14

FT /note= "At least one amino acid must have D-
 FT configuration"

XX WO9640770-A2.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009962.

XX 07-JUN-1995; 95US-00485273.

XX (PERI-) PERIODONTIX INC.

XX (UYBO-) UNIV BOSTON.

PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;

XX WPI; 1997-052234/05.

XX Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based
 PT peptide(s) - useful esp for treating Candidal infections, periodontitis
 PT and caries.

PS Claim 2; Fig 1; 63pp; English.

XX The present sequence represents a specifically claimed example of an anti-
 CC fungal and anti-bacterial D-amino acid histatin-based peptide 104, where
 CC at least one amino acid in the peptide is in the D-configuration. The
 CC peptide is preferably modified by an acetyl or carbamyl addition at the N
 CC -terminus and/or amidation at the C-terminus. The novel D-amino acid-
 CC containing peptide, based on the naturally occurring histidine-rich human
 CC histatins, have anti-fungal and anti-bacterial activity and are useful in
 CC compositions for the treatment of oral, vaginal, urethral, mucosal,
 CC respiratory, skin, ear and ophthalmic fungal or bacterial infections. It
 CC is particularly effective against local and systemic Candida albicans
 CC infection, against oral bacterial diseases such as caries and
 CC periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas
 CC gingivalis) and against Clostridium histolyticum. The D-amino acid-
 CC containing peptide has superior anti-fungal (especially anti-candidal)
 CC and anti-bacterial activity, particularly on a weight basis, compared to
 CC the natural L- amino acid forms of histatins and histatin-based peptides.
 CC The presence of D-residues also makes the peptides more resistant to
 CC degradation than corresponding L-amino acid versions

XX Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8

Db 1 GYKR-KPH 7

RESULT 44

AAW31675

ID AAW31675 standard; peptide; 14 AA.

XX AAW31675;

XX 27-MAR-1998 (first entry)

XX Human histatin 3 based peptide 3P4.

KW Histatin 3; macaque; human; treatment; fungal infection; candidiasis;
 KW histidine rich protein.

XX Synthetic.

OS Homo sapiens.

XX US5696078-A.

XX 09-DEC-1997.

PF 16-MAY-1995; 95US-00441914.

XX 01-NOV-1991; 91US-00786571.

PR 28-OCT-1993; 93US-00145030.

PR 09-AUG-1994; 94US-00287717.

XX (UYBO-) UNIV BOSTON.

XX Oppenheim FG, Xu T;

XX WPI; 1998-041326/04.

PT Treating fungal infections - by administering histatin peptide(s).

XX Claim 1; Col 11-12; 19pp; English.

XX This is a human histatin 3 based peptide 3P4. Histatin is a histidine
 CC rich salivary protein. This peptide and other peptides based on human
 CC histatin 3 and macaque histatins can be synthesised for treatment of
 CC fungal, in particular, candidal infections. Expression vectors encoding
 CC these peptides can be used in antifungal treatment methods. They can be
 CC used to treat candidiasis, fungal infections of the oral cavity, vagina,
 CC urethra and skin and systemic fungal infections

XX Sequence 14 AA;

Query Match 44.2%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8

Db 1 GYKR-KPH 7

RESULT 45

AAW49599

ID AAW49599 standard; peptide; 9 AA.

XX AAW49599;

XX 05-JUN-1998 (first entry)

XX Human leucocyte antigen DQ4 binding peptide #490.

XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
 KW autoimmune disease; chronic articular rheumatism.

XX Synthetic.

XX JP08151396-A.

XX 11-JUN-1996.

XX 28-NOV-1994; 94JP-00292657.

XX 28-NOV-1994; 94JP-00292657.

XX (TEIJ) TEIJIN LTD.

XX WPI; 1996-329479/33.

XX HLA-binding oligopeptide and an immuno:regulator contg it - used in the

PT treatment of auto:immune disease.
XX
PS Claim 4; Page 53; 61pp; Japanese.
XX
CC This peptide is an example of a peptide which binds to a human leucocyte
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
CC combinatorial library comprising the sequence AAV05953, by screening with
CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune
CC disease, or especially for treatment of viral diseases
XX
SQ Sequence 9 AA;
Query Match 43.3%; Score 26; DB 2; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GYKNSKFHR 9
Db 1 GYKRDSYER 9

Search completed: August 30, 2004, 10:49:29
Job time : 17.3885 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 200.27 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 1083

Sequence: 1 MKVLLAAALTAGSVFFLLP.....VIADCGKIEVKEPFAIKE 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	3.1	13	6 Q865C9	Q865C9 sus scrofa
2	32	3.0	13	10 Q9AU99	Q9AU99 aethionema
3	31	2.9	9	4 Q9H326	Q9H326 homo sapien
4	31	2.9	13	13 Q9PS56	Q9PS56 carassius a
5	29	2.7	13	3 P87031	P87031 saccharomyc
6	29	2.7	13	4 Q9UPE7	Q9UPE7 homo sapien
7	29	2.7	13	8 Q9T4K5	Q9T4K5 bryopsis sp
8	29	2.7	13	8 Q9THS0	Q9THS0 bryopsis sp
9	29	2.7	13	8 Q9T4K4	Q9T4K4 bryopsis sp
10	29	2.7	13	8 Q9THS2	Q9THS2 bryopsis sp
11	29	2.7	13	8 Q9T4K6	Q9T4K6 bryopsis sp
12	29	2.7	13	8 Q9T4K3	Q9T4K3 bryopsis sp
13	29	2.7	14	4 Q9UNW9	Q9UNW9 homo sapien
14	28	2.6	14	2 Q9LCS1	Q9LCS1 bacillus su
15	27	2.5	11	5 Q9UAR8	Q9UAR8 aedes aegyp
16	27	2.5	14	2 Q9R3U3	Q9R3U3 chlamydia t

17	27	2.5	14	5	Q26100	Q26100 pratylenchu
18	27	2.5	14	6	Q9N1V6	Q9N1V6 equus cabal
19	26.5	2.4	14	2	Q52636	Q52636 escherichia
20	26	2.4	10	11	Q9QVE9	Q9QVE9 mus sp. pro
21	26	2.4	12	6	Q9N2B9	Q9N2B9 gorilla gor
22	26	2.4	12	6	Q9N2B8	Q9N2B8 pongo pygma
23	26	2.4	12	6	Q9N2C0	Q9N2C0 pan troglod
24	26	2.4	12	10	Q93YC8	Q93YC8 nicotiana t
25	26	2.4	12	10	Q8GSB9	Q8GSB9 lolium pere
26	26	2.4	12	11	Q80XV4	Q80XV4 rattus sp.
27	26	2.4	12	11	Q64313	Q64313 rattus norv
28	26	2.4	13	4	Q7Z5Z6	Q7Z5Z6 homo sapien
29	26	2.4	13	13	P82848	P82848 rana pipien
30	26	2.4	14	15	Q8JDM3	Q8JDM3 human immun
31	26	2.4	14	15	Q8JDM7	Q8JDM7 human immun
32	26	2.4	14	15	Q8JDM0	Q8JDM0 human immun
33	25.5	2.4	13	8	Q9THS3	Q9THS3 bryopsis sp
34	25	2.3	9	2	Q84F20	Q84F20 bacillus su
35	25	2.3	9	8	Q85G96	Q85G96 pyrrhobryum
36	25	2.3	10	10	Q8SAC2	Q8SAC2 amblystegiu
37	25	2.3	11	2	Q47606	Q47606 escherichia
38	25	2.3	11	4	Q9C057	Q9C057 homo sapien
39	25	2.3	12	4	Q9BQ01	Q9BQ01 homo sapien
40	25	2.3	12	8	Q9XNE6	Q9XNE6 pylaiaella l
41	25	2.3	12	10	Q8H6E6	Q8H6E6 hordeum vul
42	25	2.3	12	12	Q80IG7	Q80IG7 choristoneu
43	25	2.3	13	13	Q7ZZN7	Q7ZZN7 xenopus lae
44	25	2.3	13	15	Q98YM1	Q98YM1 human immun
45	25	2.3	14	11	Q99PB8	Q99PB8 mus musculu

ALIGNMENTS

RESULT 1
ID Q865C9 PRELIMINARY; PRT; 13 AA.
AC Q865C9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Glutamine synthetase (Fragment).
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Christenson R.K.;
RT "Characterization of porcine glutamine synthetase."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216477; AAC64254.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 3.1%; Score 34; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 73 TGEKGFQYKN 82
|||:|
Db 4 TGDEPFQYKN 13

RESULT 2
ID Q9AU99 PRELIMINARY; PRT; 13 AA.
AC Q9AU99;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Chalcone synthase (Fragment).
OS Aethionema grandiflora.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Aethionema.
 OX NCBI_TaxID=72657;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RA Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.;
 RT "Phylogenetic analysis of promoter sequences from cruciferous
 plants.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249000; AAK31935.1; -
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1432 MW; 5C444963C4621AA7 CRC64;
 Query Match 3.0%; Score 32; DB 10; Length 13;
 Best Local Similarity 60.0%; Pred. NO. 2e+04;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 21 GPSAADEKKK 30
 Db 2 GPSSILDEIRK 11
 RESULT 3
 Q9H326
 ID Q9H326 PRELIMINARY; PRT; 9 AA.
 AC Q9H326;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit
 (Fragment).
 DE IDH3A.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
 RT "Structural and functional characterization of the human NAD--
 dependent isocitrate dehydrogenase alpha subunit promoter.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF157515; AAG43379.1; -
 FT NON TER 9
 SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;
 Query Match 2.9%; Score 31; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. NO. 1e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 126 GPGWVS 131
 Db 3 GPWVLS 8
 RESULT 4
 Q9PS56
 ID Q9PS56 PRELIMINARY; PRT; 13 AA.
 AC Q9PS56;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE NEUROLIN=CELL surface glycoprotein (Fragment).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 [1]
 RN
 RP SEQUENCE.
 RX MEDLINE=92250720; PubMed=1577862;
 RA Paschke K.A., Lottspeich F., Stuermer C.A.;

RT "Neurolin, a cell surface glycoprotein on growing retinal axons in the
 RT goldfish visual system, is reexpressed during retinal axonal
 RT regeneration.";
 RL J. Cell Biol. 117:863-875 (1992).
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1332 MW; 33AF8FF8CC535728 CRC64;
 Query Match 2.9%; Score 31; DB 13; Length 13;
 Best Local Similarity 44.4%; Pred. NO. 2.4e+04;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 53 IFGLFGKTV 61
 Db 4 VIGLYGETI 12
 RESULT 5
 P87031
 ID P87031 PRELIMINARY; PRT; 13 AA.
 AC P87031;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORF YGR126W (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RA Van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,
 RA Nawrocki A., Del Bino S., Goffeau A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z72912; CAA97139.2; -
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1594 MW; 2954BA87F3F8C9C8 CRC64;
 Query Match 2.7%; Score 29; DB 3; Length 13;
 Best Local Similarity 46.7%; Pred. NO. 3.6e+04;
 Matches 7; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
 QY 74 GEKGFYKNSKPHRV 88
 Db 3 GIKGF-----FHRI 11
 RESULT 6
 Q9UPE7
 ID Q9UPE7 PRELIMINARY; PRT; 13 AA.
 AC Q9UPE7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Inosine monophosphatase 2 (Fragment).
 GN IMPA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder.";
 RL Mol. Psychiatry 2:393-397 (1997).
 [2]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025882; AAD22136.1; -.
DR EMBL; AF025881; AAD22136.1; JOINED.
FT NON TER 1 1
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;

Query Match 2.7%; Score 29; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.6e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 ERPPDENF 120
| | | | |
Db 1 ERPPSHRF 8

RESULT 7
Q9T4K5 PRELIMINARY; PRT; 13 AA.
AC Q9T4K5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSSH (Fragment).
GN PSSH.
OS Bryopsis sp. C.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103786;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Krellwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170407; AAD56846.1; -.
DR EMBL; AF170383; AAD56798.1; -.
DR EMBL; AF170384; AAD56800.1; -.
DR EMBL; AF170385; AAD56802.1; -.
DR EMBL; AF170386; AAD56804.1; -.
DR EMBL; AF170387; AAD56806.1; -.
DR EMBL; AF170388; AAD56808.1; -.
DR EMBL; AF170389; AAD56810.1; -.
DR EMBL; AF170390; AAD56812.1; -.
DR EMBL; AF170391; AAD56814.1; -.
DR EMBL; AF170392; AAD56816.1; -.
DR EMBL; AF170393; AAD56818.1; -.
DR EMBL; AF170394; AAD56820.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
| | | | |
Db 4 NSGKDT 9

RESULT 8
Q9THS0 PRELIMINARY; PRT; 13 AA.
AC Q9THS0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSSH (Fragment).
GN PSSH.
OS Bryopsis sp. B.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-15-06;
RA Krellwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170406; AAD56844.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1351 MW; 2C316AF02E93A338 CRC64;

Query Match 2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
| | | | |
Db 4 NSGKDT 9

RESULT 9
Q9T4K4 PRELIMINARY; PRT; 13 AA.
AC Q9T4K4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSSH (Fragment).
GN PSSH.
OS Bryopsis sp. B.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Krellwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170405; AAD56842.1; -.
DR EMBL; AF170395; AAD56822.1; -.
DR EMBL; AF170396; AAD56824.1; -.
DR EMBL; AF170397; AAD56826.1; -.
DR EMBL; AF170398; AAD56828.1; -.
DR EMBL; AF170399; AAD56830.1; -.
DR EMBL; AF170400; AAD56832.1; -.
DR EMBL; AF170401; AAD56834.1; -.
DR EMBL; AF170402; AAD56836.1; -.
DR EMBL; AF170403; AAD56838.1; -.
DR EMBL; AF170404; AAD56840.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

```

```

Query Match          2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
DB 4 NSGKDT 9

RESULT 10
Q9THS2 ID Q9THS2 PRELIMINARY; PRT; 13 AA.
AC Q9THS2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PSH (Fragment).
GN PSH.
OS Bryopsis sp. D.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.
OX NCBi_TaxID=103787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-07-01;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
AT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170382; AAD56796.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match          2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
DB 4 NSGKDT 9

RESULT 11
Q9THK6 ID Q9THK6 PRELIMINARY; PRT; 13 AA.
AC Q9THK6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PSH (Fragment).
GN PSH.
OS Bryopsis sp. A.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.
OX NCBi_TaxID=103784;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
AT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170415; AAD56862.1; -.
DR EMBL; AF170408; AAD56848.1; -.
DR EMBL; AF170409; AAD56850.1; -.
DR EMBL; AF170410; AAD56852.1; -.
DR EMBL; AF170411; AAD56854.1; -.

```

```

DR EMBL; AF170412; AAD56856.1; -.
DR EMBL; AF170414; AAD56860.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match          2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
DB 4 NSGKDT 9

RESULT 12
Q9THK3 ID Q9THK3 PRELIMINARY; PRT; 13 AA.
AC Q9THK3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PSH (Fragment).
GN PSH.
OS Bryopsis sp. E.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.
OX NCBi_TaxID=103788;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-05-03, 96-07-03, 95-12-02, 94-19-1R, 97-13-1R, and 98-08-03;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
AT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170380; AAD56792.1; -.
DR EMBL; AF170373; AAD56778.1; -.
DR EMBL; AF170375; AAD56782.1; -.
DR EMBL; AF170376; AAD56784.1; -.
DR EMBL; AF170377; AAD56786.1; -.
DR EMBL; AF170378; AAD56788.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match          2.7%; Score 29; DB 8; Length 13;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 134 NAGKDT 139
DB 4 NSGKDT 9

RESULT 13
Q9UNM9 ID Q9UNM9 PRELIMINARY; PRT; 14 AA.
AC Q9UNM9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RING3 protein (Fragment).
GN RING3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBi_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Keddache M, Zhang F, Greenberg D.A.;
RT "A Dinucleotide Repeat Between Exons 2 and 3 of the Human RING3
RT Gene";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107699; AAD24963.1; -;
DR InterPro; IPR001487; Bromodomain.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1677 MW; 5CDF036680AE22D3 CRC64;

Query Match 2.7%; Score 29; DB 4; Length 14;
Best Local Similarity 41.7%; Pred. No. 4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 85 FHRVVKDFMIQ 96
: : : : :
Db 2 YHKIKQPMDMG 13

RESULT 14
Q9LCS1 PRELIMINARY; PRT; 14 AA.
ID Q9LCS1
AC Q9LCS1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Levan sucrase (Fragment).
DE SABC.
GN Bacillus subtilis.
OS Plasmid p1257.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
SEQUENCE FROM N.A.
RA Maldonado R.; Casades J.;
RT "Identification of IS210 in Azotobacter vinelandii: a novel,
RT functional insertion element member of the IS5 family.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249381; CAB76429.1; -;
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1623 MW; 8DC9108BA1B18745 CRC64;

Query Match 2.6%; Score 28; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 4.9e+04;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 178 KTDSDKPLKD 188
: : : : :
Db 1 KFDANDSILKD 11

RESULT 15
Q9UAR8 PRELIMINARY; PRT; 11 AA.
ID Q9UAR8
AC Q9UAR8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sialokinin I preproprotein (Fragment).
OS Aedes aegypti (yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
RX MEDLINE=20099025; PubMed=10620041;
RA Beertsen B.T.; Champagne D.E.; Coleman J.L.; Campos Y.A.; James A.A.;
RT "Characterization of the Sialokinin I gene encoding the salivary
RT vasodilator of the yellow fever mosquito, Aedes aegypti.";

RL Insect Mol. Biol. 8:459-467(1999).
DR EMBL; AF108100; AAD16884.1; -;
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 11 AA; 1203 MW; 8BADCT77C6B59C33A CRC64;

Query Match 2.5%; Score 27; DB 5; Length 11;
Best Local Similarity 45.5%; Pred. No. 4.4e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 48 DVGGRVIFGLFG 58
: : : : :
Db 1 DTGDKFYGLMG 11

RESULT 16
Q9R3U3 PRELIMINARY; PRT; 14 AA.
ID Q9R3U3
AC Q9R3U3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 27 kDa histone analog (Fragment).
DE Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
SEQUENCE.
RX MEDLINE=92041597; PubMed=1938908;
RA Hackstadt T.;
RT "Purification and N-terminal amino acid sequences of Chlamydia
RT trachomatis histone analogs.";
RL J. Bacteriol. 173:7046-7049(1991).
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1519 MW; 423ED67AE4969D03 CRC64;

Query Match 2.5%; Score 27; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6e+04;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 171 VRKVESTKT 179
: : : : :
Db 4 VQKRSITKT 12

RESULT 17
Q26100 PRELIMINARY; PRT; 14 AA.
ID Q26100
AC Q26100
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Pmsp-5 (Fragment).
GN PMSp-5.
OS Pratylenchus penetrans (Root-lesion nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
OX NCBI_TaxID=45929;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Maryland isolate;
RA Setterquist R.A.; Smith G.K.; Jones R.; Fox G.E.;
RT "Diagnostic Probes Targeting the Major Sperm Protein Gene may be
RT Useful for the Molecular Identification of Nematodes.";
RL J. Nematol. 0:0-0(1996).
DR EMBL; U57830; AAB02263.1; -;
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1775 MW; 18EB70A35334554B CRC64;

Query Match 2.5%; Score 27; DB 5; Length 14;
 Best Local Similarity 36.4%; Pred. No. 6e+04;
 Matches 4; Conservative 3; Mismatches 0; Gaps 0;

QY 155 DGKHVFGKVL 165
 DB 2 DDKHTYMKII 12

RESULT 18
 Q9N1V6 PRELIMINARY; PRT; 14 AA.
 AC Q9N1V6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Beta-hemoglobin (Fragment).
 GN HBB.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20082971; PubMed=10613847;
 RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
 RA Bowling A.T., Murray J.D.;
 RT "A comparative gene map of the horse (Equus caballus).";
 RL Genome Res. 9:1239-1249(1999).
 DR EMBL; AF134224; AAF63865.1; -.
 FT NON_TER 1 1
 FT 14 14
 SQ SEQUENCE 14 AA; 1456 MW; 5C14536E1EBF1977 CRC64;

Query Match 2.5%; Score 27; DB 6; Length 14;
 Best Local Similarity 40.0%; Pred. No. 6e+04;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 44 IGDEDVGRVI 53
 DB 2 VGGEALGRLV 11

RESULT 19
 Q52636 PRELIMINARY; PRT; 14 AA.
 ID Q52636;
 AC Q52636;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Tral protein (Fragment).
 GN TRAL.
 OS Escherichia coli.
 OG Plasmid R124.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86059219; PubMed=2999074;
 RA Frost L.S., Finlay B.B., Oppenorth A., Paranchych W., Lee J.S.;
 RT "Characterization and sequence analysis of pilin from F-like
 Tral plasmids";
 RL J. Bacteriol. 164:1238-1247(1985).
 DR EMBL; K03092; AAA92759.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1713 MW; 5CCA91188E30E23 CRC64;

Query Match 2.4%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 77.8%; Pred. No. 6.6e+04;
 Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 117 DENFKLKH 125
 DB 4 DEN-KLKX 11

RESULT 20
 Q9QVE9 PRELIMINARY; PRT; 10 AA.
 ID Q9QVE9;
 AC Q9QVE9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Protamine MP2 intermediate protein PMP2/11 (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92174934; PubMed=1541289;
 RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
 RT "Molecular characterization of six intermediate proteins in the
 processing of mouse protamine P2 precursor";
 RL Eur. J. Biochem. 204:759-765(1992).
 FT NON_TER 1 1
 FT 10 10
 SQ SEQUENCE 10 AA; 1029 MW; FCAD2DD8676866D1 CRC64;

Query Match 2.4%; Score 26; DB 11; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.7e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPG 128
 DB 3 HQGPG 7

RESULT 21
 Q9N2B9 PRELIMINARY; PRT; 12 AA.
 ID Q9N2B9;
 AC Q9N2B9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Indolethylamine N-methyltransferase (Fragment).
 GN INMT.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gorilla-UI.
 RA Kitano T., Kobayakawa H., Saitou N.;
 RT "Silver Project";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB041364; BA94453.1; -.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Methyltransferase; Transferase.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 2.4%; Score 26; DB 6; Length 12;
 Best Local Similarity 71.4%; Pred. No. 6e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
 DB 3 GGFTGGD 9

```
RESULT 22
Q9N2B8      PRELIMINARY;      PRT;      12 AA.
AC
Q9N2B8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN INMT.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=oran-Pol3;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041365; BAA94454.1; -.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1230 MW; CF079554917861A9 CRC64;

Query Match      2.4%; Score 26; DB 6; Length 12;
Best Local Similarity 71.4%; Pred. No. 6e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
DB 3 GGFTGGD 9

RESULT 23
Q9N2C0      PRELIMINARY;      PRT;      12 AA.
AC
Q9N2C0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN INMT.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=chimp-220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041363; BAA94452.1; -.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match      2.4%; Score 26; DB 6; Length 12;
Best Local Similarity 71.4%; Pred. No. 6e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
DB 3 GGFTGGD 9

RESULT 24
Q93YC8      PRELIMINARY;      PRT;      12 AA.
ID
Q93YC8
```

```
AC
Q93YC8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coat protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC van der Winden J.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=20027532; PubMed=10557305;
RA Jakowitsch J., Mette M.F., van der Winden J., Matzke M.A.,
RA Matzke A.J.;
RT "Integrated pararetroviral sequences define a unique class of
RT dispersed repetitive DNA in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).
DR EMBL; AJ414170; CAC88799.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1402 MW; 89226B3A0351E321 CRC64;

Query Match      2.4%; Score 26; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 6e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 KHYG 126
DB 6 KHYG 9

RESULT 25
Q8GSB9      PRELIMINARY;      PRT;      12 AA.
ID
Q8GSB9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENOD40-like protein.
OS Lolium perenne (perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Borvi; TISSUE=stem;
RA Larsen K.;
RT "ENOD40 homolog from perennial ryegrass (Lolium perenne).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Larsen K.;
RT "ENOD40 gene from perennial ryegrass (Lolium perenne).";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538350; AAN15133.1; -.
DR EMBL; AF538351; AAN15134.1; -.
SQ SEQUENCE 12 AA; 1455 MW; 3EF4B0A918EB1733 CRC64;

Query Match      2.4%; Score 26; DB 10; Length 12;
Best Local Similarity 40.0%; Pred. No. 6e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 149 VKTAWLDGKH 158
DB 149 VKTAWLDGKH 158
```

Db 1 MEDAWLEHLH 10

RESULT 26

Q80XV4 PRELIMINARY; PRT; 12 AA.

AC Q80XV4; DB 12; Length 12;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Orf4.

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94012815; PubMed=8408077;

RA Rao S.M., Howells R.D.;

RT "cis-acting elements in the 5'-untranslated region of rat testis

RT proenkephalin mRNA regulate translation of the precursor protein.";

RL J. Biol. Chem. 268:22164-22169(1993).

DR EMBL: S66180; AAP13974.1;

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

Query Match 2.4%; Score 26; DB 11; Length 12;

Best Local Similarity 66.7%; Pred. No. 6e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 153 WLDGKH 158

Db 7 WDSGKH 12

RESULT 27

Q64313 PRELIMINARY; PRT; 12 AA.

AC Q64313; DB 12; Length 12;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN ENK.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Fisher 344; TISSUE=Striatum;

RX MEDLINE=90066445; PubMed=2573832;

RA Garrett J.E., Collard M.W., Douglass J.O.;

RT "Translational control of germ cell-expressed mRNA imposed by

RT alternative splicing: opioid peptide gene expression in rat testis.";

PL Mol. Cell. Biol. 9:4381-4389(1989).

DR EMBL: K02805; AAA60733.1;

RW Hypothetical protein.

SQ SEQUENCE 12 AA; 1436 MW; D33C6D2A83B36776 CRC64;

Query Match 2.4%; Score 26; DB 11; Length 12;

Best Local Similarity 66.7%; Pred. No. 6e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 153 WLDGKH 158

Db 7 WDSGKH 12

RESULT 28

Q725Z6 PRELIMINARY; PRT; 13 AA.

ID Q725Z6; DB 13; Length 13;

AC Q725Z6; DB 13; Length 13;

DT 01-OCT-2003 (TREMBLrel. 25, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE NPC-A-11

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Shu J., Li G., He X.;

RT "Construction of cDNA expression library from nasopharyngeal carcinoma

RT tissue and screening of antigenic genes.";

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY320404; AAP73806.1;

SQ SEQUENCE 13 AA; 1429 MW; 1D0C143838017694 CRC64;

Query Match 2.4%; Score 26; DB 4; Length 13;

Best Local Similarity 71.4%; Pred. No. 6.6e+04;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 131 SWANAGK 137

Db 3 SLANWGK 9

RESULT 29

P82848 PRELIMINARY; PRT; 13 AA.

ID P82848; DB 13; Length 13;

AC P82848; DB 13; Length 13;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Temporin-1P.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.

OX NCBI_TaxID=8404;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=SKIN;

RX MEDLINE=20117700; PubMed=10651828;

RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,

RA Conlon J.M.;

RT "Peptides with antimicrobial activity from four different families

RT isolated from the skins of the North American frogs Rana luteiventris,

RT Rana berlandieri and Rana pipiens.";

RL Eur. J. Biochem. 267:894-900(2000).

CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM

CC S.AUREUS.

CC -!- MASS SPECTROMETRY: MW=1368; METHOD=ELECTROSPRAY.

CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN

CC FAMILY.

DR GO: GO:0006805; P: xenobiotic metabolism; IEA.

KW Antibiotic; Amidation.

FT MOD RES 13 13

SQ SEQUENCE 13 AA; 1370 MW; 3EF3402B9DF92338 CRC64;

Query Match 2.4%; Score 26; DB 13; Length 13;

Best Local Similarity 44.4%; Pred. No. 6.6e+04;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 160 VFGKVLQGM 168

Db 4 IVGKLLSGL 12

RESULT 30

Q8JDM3 PRELIMINARY; PRT; 14 AA.

ID Q8JDM3; DB 14; Length 14;

AC Q8JDM3; DB 14; Length 14;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

```
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalia K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576 (2002).
DR EMBL; AF407149; AM66202.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 2.4%; Score 26; DB 15; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.2e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTG 106
Db 6 RGDPTG 11

RESULT 31
Q8JDM7 PRELIMINARY; PRT; 14 AA.
AC Q8JDM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalia K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576 (2002).
DR EMBL; AF407148; AM66198.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 2.4%; Score 26; DB 15; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.2e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTG 106
Db 6 RGDPTG 11

RESULT 32
Q8JDM0 PRELIMINARY; PRT; 14 AA.
AC Q8JDM0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=22032414; PubMed=12036486;
RA Long E.M., Rainwater S.M., Lavreys L., Mandalia K., Overbaugh J.;
RT "HIV Type 1 Variants Transmitted to Women in Kenya Require the CCR5
RT Coreceptor for Entry, Regardless of the Genetic Complexity of the
RT Infecting Virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576 (2002).
DR EMBL; AF407150; AM66205.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 2.4%; Score 26; DB 15; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.2e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTG 106
Db 6 RGDPTG 11

RESULT 33
Q9THS3 PRELIMINARY; PRT; 13 AA.
AC Q9THS3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PSH (Fragment).
GN PSH.
OS Bryopsis sp. D.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaes;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-21-02;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170381; AAD56794.1; -.
RG GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1379 MW; 2C31687A3B73A338 CRC64;

Query Match 2.4%; Score 25.5; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 7.3e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 134 NAGKDTNG 141
Db 4 NSGKD-NG 10

RESULT 34
Q84F20 PRELIMINARY; PRT; 9 AA.
AC Q84F20;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89034018; PubMed=2460441;
RA Nakamura K., Itoh Y., Yamane K.;
RT "Enhanced secretion of beta-lactamase on structural modification of
RT the Bacillus subtilis alpha-amylase signal peptide.";
```

RL J. Biochem. 104:265-269(1988).
 DR EMBL; D13786; BAC56113.1; -.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 728 MW; C6B9BDDDDDC7687D CRC64;

Query Match 2.3%; Score 25; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 19 LPGPSAA 25
 Db |||:|
 1 LAGPAAA 7

RESULT 35
 Q85G96 PRELIMINARY; PRT; 9 AA.
 ID Q85G96;
 AC Q85G96;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE AtpB (Fragment).
 CN AtpB.
 OS Pyrrhobryum mnioides.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Rhizogoniales; Rhizogoniaceae; Pyrrhobryum.
 OX NCBI_TaxID=129293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22569835; PubMed=12683518;
 RA McDaniel S.F., Shaw A.J.;
 RT "Phylogeographic structure and cryptic speciation in the trans-
 Antarctic moss Pyrrhobryum mnioides.";
 RL Evolution 57:205-215(2003).
 DR EMBL; AY143022; AAN52447.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1042 MW; 4040D1B415BAB1A3 CRC64;

Query Match 2.3%; Score 25; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 KTDSR 182
 Db |||:|
 2 KTDSR 6

RESULT 36
 Q8SAC2 PRELIMINARY; PRT; 10 AA.
 ID Q8SAC2;
 AC Q8SAC2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE AtpB (Fragment).
 OS Amblystegium varium
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
 OX NCBI_TaxID=111436;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AVaa;
 RA Vanderpoorten A., Shaw A.J., Cox C.J.;
 RT "Reconciled gene trees, molecular evolution, and species relationships
 in Amblystegium (Bryopsida).";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF464972; AAL75469.1; -.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1143 MW; 9D5040D1B415BAB1 CRC64;

Query Match 2.3%; Score 25; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+04;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 KTDSR 182
 Db |||:|
 2 KTDSR 6

RESULT 37
 Q47606 PRELIMINARY; PRT; 11 AA.
 ID Q47606;
 AC Q47606;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REase.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 modification systems.";
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63622; AAA24562.1; -.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 2.3%; Score 25; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 6.5e+04;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 197 IEVEKPF 203
 Db |||:|
 1 MEVEKEF 7

RESULT 38
 Q9C057 PRELIMINARY; PRT; 11 AA.
 ID Q9C057;
 AC Q9C057;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HEX (Fragment).
 GN HEX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;
 RT "Human Hex 5'-flanking sequence.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF182950; AAK12833.1; -.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1125 MW; 2644D7FE686761F7 CRC64;

Query Match 2.3%; Score 25; DB 4; Length 11;
 Best Local Similarity 80.0%; Pred. No. 6.5e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 20 PGPSA 24
 Db |||:|
 6 PGPA 10

```
RESULT 39
Q9BQQ1 ID Q9BQQ1 PRELIMINARY; PRT; 12 AA.
AC Q9BQQ1 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BA28009.2.2 (Novel protein (Isoform 3)) (Fragment).
GN DUB3IM13.5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Llyod D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121582; CAC36069.1; -.
FT NON TER 1 1
SQ SEQUENCE 12 AA; 1017 MW; 4789B7218E787877 CRC64;

Query Match 2.3%; Score 25; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 7.3e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 104 GTGGKS 109
DB 7 GGGGKS 12

RESULT 40
Q9XNR6 ID Q9XNR6 PRELIMINARY; PRT; 12 AA.
AC Q9XNR6 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
GN NAD3.
OS Pylaiella littoralis.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pylaiella.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RA Oudot M.P., Kloareg B., Loiseaux-de Goer S.;
RL MEDLINE=99346148; PubMed=10415341;
RT "The mitochondrial Pylaiella littoralis nad1 gene contains only the
N-terminal FeS-binding domain.";
RL Gene 235:131-137(1999).
DR EMBL; AF110139; AAD44051.1; -.
GO GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion; Ubiquinone.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match 2.3%; Score 25; DB 8; Length 12;
Best Local Similarity 45.5%; Pred. No. 7.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 120 FKLKHGPGWV 130
DB 2 FLLKEYTPALI 12

RESULT 41
Q8H6E6 ID Q8H6E6 PRELIMINARY; PRT; 12 AA.
AC Q8H6E6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
```

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ENOD40-like protein.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Orthega;
RC Larsen K.;
RT "ENOD40 homologue from barley (Hordeum vulgare).";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF542513; AAN28683.1; -.
SQ SEQUENCE 12 AA; 1367 MW; 3EEABFA918EB1733 CRC64;

Query Match 2.3%; Score 25; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 7.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 152 AWLDGKH 158
DB 4 AWLEHLH 10

RESULT 42
Q80IG7 ID Q80IG7 PRELIMINARY; PRT; 12 AA.
AC Q80IG7 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mini-cistron protein.
OS Choriostoeura fumiferana nuclear polyhedrosis virus (CFMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=208973;
RN [1]
RP SEQUENCE FROM N.A.
RA Carstens E.B.;
RT "Identification and analysis of the CFMNPV P143 gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127530; AAF36457.1; -.
SQ SEQUENCE 12 AA; 1252 MW; C878D87A89B2CDD9 CRC64;

Query Match 2.3%; Score 25; DB 12; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.3e+04;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 55 GLFGKTVPKT 64
DB 3 GGFVTTPT 12

RESULT 43
Q7ZZN7 ID Q7ZZN7 PRELIMINARY; PRT; 13 AA.
AC Q7ZZN7 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Zinc finger protein (Fragment).
GN ZIC3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Cerebellum;
RA Weber J.R., Sokol S.Y.;
```

RT "Identification of a phylogenetically conserved activin-responsive
RT enhancer in the Zic3 gene."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506277; AAP20808.1; -
FT NON_TER 1 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1569 MW; 819B7A159F531861 CRC64;

Query Match 2.3%; Score 25; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 8e+04; 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 TGEKGF 78
Db |||||
6 TGEKPF 11

RESULT 44

ID Q98YMI PRELIMINARY; PRT; 13 AA.
AC Q98YMI;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=991043;
RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
RA Korn K.;
RT "Recovery of HIV-1 pol gene sequences by direct sequencing of
RT amplification products derived from plasma samples."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF347446; AAK32523.1; -
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1390 MW; 805408704623D1AA CRC64;

Query Match 2.3%; Score 25; DB 15; Length 13;
Best Local Similarity 38.5%; Pred. No. 8e+04;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 178 KTDSDKPLKVI 190
Db :|:|:|:|:|
1 ETGDDTVLEDII 13

RESULT 45

ID Q99PB8 PRELIMINARY; PRT; 14 AA.
AC Q99PB8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Adenosine kinase (EC 2.7.1.20) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Singh B., Lin A., Wu Z.-C., Gupta R.S.;
RT "Gene Structure for Adenosine Kinase in Chinese Hamster and Human:
RT High Frequency Mutants of CHO cells involve deletions of several
RT introns and exons."
RL DNA Cell Biol. 0:0-0(2001).
DR EMBL; AF318953; AAK07186.1; -
DR GO; GO:0004001; F:adenosine kinase activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

KW Kinase; Transferase.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1526 MW; 27863376667D5A27 CRC64;

Query Match 2.3%; Score 25; DB 11; Length 14;
Best Local Similarity 63.6%; Pred. No. 8.8e+04;
Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 23 SAADEKKKGPK 33
Db :|||:|:|
2 AAADEPK--PK 10

Search completed: August 30, 2004, 10:55:31
Job time : 201.27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 35.9378 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 1083

Sequence: 1 MKVLLAAALAGSVFFLLP.....VIIADCGKIEVEKPPAIKAE 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	3.7	14	1 EFTU CANFA	P54835 canis famil
2	30	2.8	10	1 PAPI_PARMA	P81863 pardachirus
3	30	2.8	11	1 CA31_LITCI	P82089 litoria cit
4	30	2.8	11	1 GER2_HORVU	P28526 hordeum vul
5	29	2.7	11	1 CA32_LITCI	P82090 litoria cit
6	29	2.7	13	1 GER1_HORVU	P28525 hordeum vul
7	29	2.7	14	1 TAT_HV1W2	P12509 human immun
8	29	2.7	14	1 TAT_HV1Z8	P12511 human immun
9	28	2.6	8	1 RPCH_PANBO	P08939 pandalus bo
10	28	2.6	10	1 HTP_NAUCI	P10939 nauphoeta c
11	28	2.6	13	1 LPAA_PORGI	P81411 porphyromon
12	27	2.5	9	1 AL11_CARMA	P81814 carcinus ma
13	27	2.5	10	1 GONL_SQUAC	P27429 squallus aca
14	27	2.5	13	1 CRBL_VESMA	P17232 vespa manda
15	27	2.5	13	1 CRBL_VESTR	P17231 vespa tropi
16	27	2.5	13	1 TEMF_RANTE	P56921 rana tempor
17	26.5	2.4	12	1 TKN_KASSE	P08611 kassina sen
18	26	2.4	10	1 GON2_CHICK	P37043 gallus gall
19	26	2.4	10	1 GON3_ONCKE	P20367 oncorhynch
20	26	2.4	12	1 F1P1_SARBU	P83349 sarcophaga
21	26	2.4	13	1 TEMA_RANTE	P56917 rana tempor
22	26	2.4	14	1 CRBL_VESOR	P17236 vespa orien
23	26	2.4	14	1 F1BB_MANLE	P14474 mandrillus
24	25	2.3	8	1 AKH_MELML	P25423 melolontha
25	25	2.3	8	1 AKH_TABAT	P14595 tabanus atr
26	25	2.3	10	1 HTP_TABAT	P14596 tabanus atr
27	25	2.3	10	1 SLAP_BACTG	P49325 bacillus th
28	25	2.3	11	1 R330_ONCMY	P83328 oncorhynch
29	25	2.3	12	1 HS9A_RAT	P82995 rattus norv
30	24.5	2.2	13	1 T1A3_TREME	P01370 tremella me
31	24	2.2	10	1 BRK_ONCMY	Q9prz1 oncorhynch
32	24	2.2	10	1 CAER_LITXA	P56264 litoria xan
33	24	2.2	10	1 TKS1_AEDAE	P42634 aedes aegyp

34	24	2.2	10	1 TKS1_AEDAE	P42635 aedes aegyp
35	24	2.2	13	1 HPB3_RANES	P32416 rana esculi
36	23.5	2.2	12	1 RFL_CONSP	P58805 conus spuri
37	23.5	2.2	14	1 UN46_CLOPA	P81362 clostridium
38	23	2.1	8	1 LMT2_LOCOMI	P22396 locusta mig
39	23	2.1	10	1 COXO_RAT	P80432 rattus norv
40	23	2.1	10	1 COXO_THUOB	P80982 thunnus obe
41	23	2.1	10	1 URA7_HUMAN	P34990 homo sapien
42	23	2.1	11	1 CORZ_PPARAM	P11496 periplaneta
43	23	2.1	11	1 TKN4_PSEGU	P42989 pseudophryn
44	23	2.1	13	1 ADFE_TENMO	P83109 tenebrio mo
45	23	2.1	14	1 MAST_VESCR	P01516 vespa crabr

ALIGNMENTS

RESULT 1					
ID	EFTU CANFA	STANDARD;	PRT;	14 AA.	
AC	P54835;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Elongation factor Tu, mitochondrial (EF-Tu) (Fragment).				
GN	TUFM.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Heart;				
RX	MEDLINE=98163340; PubMed=9504812;				
RA	Dunn M.J., Corbett J.M., Wheeler C.H.;				
RT	"HSC-2DPAGE and the two-dimensional gel electrophoresis database of				
RT	dog heart proteins.";				
RL	Electrophoresis 18:2795-2802(1997).				
CC	-!- FUNCTION: This protein promotes the GTP-dependent binding of				
CC	aminoacyl-tRNA to the A-site of ribosomes during protein				
CC	biosynthesis.				
CC	-!- SUBCELLULAR LOCATION: Mitochondrial.				
CC	-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.				
CC	EF-Tu/EF-1A subfamily.				
DR	HSC-2DPAGE; P54835; DOG.				
DR	InterPro; IPR000795; EF_GTPbind.				
DR	PROSITE; PS00301; EFACFOR GTP; PARTIAL.				
KW	Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding.				
FT	NON TER	14			
SQ	SEQUENCE	14 AA; 1600 MW; 8CAF0B6AE7CCDE41 CRC64;			
Query Match 3.7%; Score 40; DB 1; Length 14;					
Best Local Similarity 61.5%; Pred. No. 8.4e+02;					
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
Qy	174 VESTKTDSDKPL 186				
	: :				
Db	2 VEAKTYVRDKPI 14				
RESULT 2					
ID	PAPI_PARMA	STANDARD;	PRT;	10 AA.	
AC	P81863;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Pardaxin I (PXI) (Fragment).				
OS	Pardachirus marmoratus (Red sea mosses sole).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;				
OC	Soleoidei; Soleidae; Pardachirus.				

OX NCBI_TaxID=31087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=87057369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 RT "Purification and pore-forming activity of two hydrophobic
 peptide fragments from the secretion of the Red sea moses sole (*Pardachirus
 marmoratus*).";
 RL J. Biol. Chem. 261:16704-16713(1986).
 CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
 properties. Forms voltage-dependent, ion-permeable channels in
 membranes. At high concentration causes cell membrane lysis. Shown
 to be 5-10 times more toxic, cytolytic and active in membrane pore
 formation than pardaxin II.
 CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pardaxin family.
 KW Toxin.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1063 MW; D399C36760572DD9 CRC64;

 Query Match 2.8%; Score 30; DB 1; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4.6e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 OX 15 FFLLPLPG 21
 Db [1]
 2 FFALPLPG 8

 RESULT 3
 CA31_LITCI STANDARD; PRT; 11 AA.
 ID CA31_LITCI
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 sulfated.
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KY Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

 Query Match 2.8%; Score 30; DB 1; Length 11;
 Best Local Similarity 66.7%; Pred. No. 5.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OX 125 YGPGWV 130
 Db [1]
 4 YGTGWM 9

 RESULT 4
 GER2_HORVU STANDARD; PRT; 13 AA.
 ID GER2_HORVU
 AC P28526;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Germin GS2 (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. CM 72; TISSUE=Root;
 RA Harkman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt
 stress.";
 RL Plant Physiol. 97:366-374(1991).
 CC -!- FUNCTION: May play a role in altering the properties of cell walls
 during germinative growth.
 CC -!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
 CC -!- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the
 mature region, but not in the tip. Not detected in leaves.
 CC -!- INDUCTION: Increased by salt stress in roots and decreased by salt
 stress in coleoptile.
 CC -!- PTM: Glycosylated.
 CC -!- SIMILARITY: Belongs to the germin family.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN; PARTIAL.
 KW Apoplast; Cell wall; Glycoprotein; Multigene family.
 FT NON_TER 10 10
 FT UNSURE 13 13
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7B6D7 CRC64;

 Query Match 2.8%; Score 30; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.1e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 OX 185 PLQDVIAD 193
 Db [1]
 5 PLQDFCIAD 13

 RESULT 5
 CA32_LITCI STANDARD; PRT; 11 AA.
 ID CA32_LITCI
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 using electrospray mass spectrometry.";

```

RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -|- FUNCTION: Hypotensive neuropeptide (Probable).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin dorsal glands.
CC -|- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -|- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -|- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC InterPro: IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A96B CRC64;

Query Match 2.7%; Score 29; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 6.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 YGPGW 129
Db 4 YGTGW 8

RESULT 6
GER1_HORVU
ID -GER1_HORVU STANDARD; PRT; 13 AA.
AC P28525;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Germin GSI (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RN SEQUENCE.
RC STRAIN=cv. CM 72; TISSUE=Root;
RA Harkman W.J., Tao H.P., Tanaka C.K.;
RT "Germin-like polypeptides increase in barley roots during salt
RT stress.";
RL Plant Physiol. 97:366-374(1991).
CC -|- FUNCTION: May play a role in altering the properties of cell
CC walls during germinative growth.
CC -|- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
CC (By similarity).
CC -|- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
CC -|- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in
CC the mature region, but not in the tip. Not detected in leaves.
CC -|- INDUCTION: Increased by salt stress in roots and decreased by salt
CC stress in coleoptile.
CC -|- PTM: Glycosylated.
CC -|- SIMILARITY: Belongs to the germin family.
CC InterPro: IPR001929; Germin.
DR PROSITE; PS00725; GERMIN; PARTIAL.
KW Apoplast; Cell wall; Glycoprotein; Multigene family.
FT UNSURE 10 10
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7B6D7 CRC64;

Query Match 2.7%; Score 29; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 7.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 185 PLKDVITAD 193
Db 5 PLQDFCVAD 13

```

```

RESULT 7
TAT_HVLW2
ID -TAT_HVLW2 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553(1986).
CC -|- FUNCTION: transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -|- SUBUNIT: Binds cyclin T1 (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -|- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M12507; AAB12991.1; --
DR HIV; M12507; TAT$WMJ2.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BEEF67AA8 CRC64;

Query Match 2.7%; Score 29; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.1e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 101 RGDGTGCK 108
Db 6 RGDPTGPK 13

RESULT 8
TAT_HVLZ8
ID -TAT_HVLZ8 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=86281278; PubMed=3395517;
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";

```

```

RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -!- SUBUNIT: Binds cyclin T1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE 2-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J03653; AAA44685.1; -.
CC HIV; J03653; TAT3Y1.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
CC AIDS.
CC FT NON_TER 1 1
CC SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;
CC -----
CC Query Match 2.7%; Score 29; DB 1; Length 14;
CC Best Local Similarity 75.0%; Pred. No. 8.1e+03;
CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC -----
QY 101 RGDGTGGK 108
DQ |||||
DB 6 RGDPTGPK 13

RESULT 9
RPCH_PANBO
ID RPCH_PANBO STANDARD; PRT; 8 AA.
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC Pandallidae; Pandalus.
OX NCBI_TaxID=6703;
RN [1]
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=4433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
RT Pandalus borealis."
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -!- FUNCTION: This hormone adapts the animal to light backgrounds by
CC stimulating concentration of the pigment of its red body-
CC chromatophores.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
CC PIR; A61348; A61348.
CC IncerPro; IPR002047; AKH.
CC PROSITE; PS00256; AKH; 1.
CC KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
CC FT MOD_RES 1 1
CC FT MOD_RES 8 8
CC SQ SEQUENCE 8 AA; 948 MW; 86786775B9C4736 CRC64;
CC -----
CC Query Match 2.6%; Score 28; DB 1; Length 8;
CC Best Local Similarity 50.0%; Pred. No. 1.4e+05;
CC Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 124 HYGPGW 129
DQ ::|||
DB 3 NFSPGW 8

Query Match 2.6%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
-----
QY 124 HYGPGW 129
DQ ::|||
DB 3 NFSPGW 8

RESULT 11
LPAA_PORGI

```

```

Db 3 NFSPGW 8

RESULT 10
HTF_NAUCI
ID HTF_NAUCI STANDARD; PRT; 10 AA.
AC P10319;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosemic hormone (HTH) (Hypertrehalosemic neuropeptide).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Leucophaea maderae (Madeira cockroach),
OS Blattella germanica (German cockroach), and
OS Gromphadorina portentosa (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Nauphoeta.
OX NCBI_TaxID=6990, 6988, 6973, 36953;
RN [1]
RP SEQUENCE.
RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
RX MEDLINE=871100208; PubMed=3801028;
RA Gaede G., Rinehart K.L. Jr.;
RT "Amino acid sequence of a hypertrehalosemic neuropeptide from the
RT corpus cardiaca of the cockroach, Nauphoeta cinerea."
RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
RN [2]
RP SEQUENCE.
RC SPECIES=L.maderae, G.portentosa, and B.germanica;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP SEQUENCE.
RC SPECIES=B.germanica;
RX MEDLINE=91179584; PubMed=2080017;
RA Veenstra J.A., Camps F.;
RT "Structure of the hypertrehalosemic neuropeptide of the German
RT cockroach, Blattella germanica."
RL Neuropeptides 15:107-109(1990).
CC -!- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
CC PIR; A26381; A26381.
CC PIR; A60421; A60421.
CC PIR; S08997; S08997.
CC PIR; S08998; S08998.
CC InterPro; IPR002047; AKH.
CC PROSITE; PS00256; AKH; 1.
CC KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
CC FT MOD_RES 1 1
CC FT MOD_RES 10 10
CC SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;
CC -----
CC Query Match 2.6%; Score 28; DB 1; Length 10;
CC Best Local Similarity 50.0%; Pred. No. 6.9e+03;
CC Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC -----
QY 124 HYGPGW 129
DQ ::|||
DB 3 NFSPGW 8

Query Match 2.6%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
-----
QY 124 HYGPGW 129
DQ ::|||
DB 3 NFSPGW 8

RESULT 11
LPAA_PORGI

```

RESULT 12
ID LPAA_PORGI STANDARD; PRT; 13 AA.
AC P81411;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Lipid-A-associated protein (Fragment)
OS Porphyromonas gingivalis (Bacteroides gingivalis)
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
ON NCBI_TaxID=837;
RN [1]
RP SEQUENCE
RC STRAIN=W50;
RX MEDLINE=99061194; PubMed=9846737;
RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
RA Curtis L., Henderson B., Tabona P.;
RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
RT from the haemagglutinating domain of the RI protease gene family, is
RT a potent stimulator of interleukin 6 synthesis."
RL Microbiology 144:3019-3026(1998).
CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
CC THAT ANCHORS THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
CC CELL.
CC VARIANT 12 12 G -> F.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;
Query Match 2.6%; Score 28; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 9.1e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 134 NAGKDTGNS 142
| | | | |
DB 5 NPDKDTGDN 13

RESULT 12
ALIL_CARMA
ID ALIL_CARMA STANDARD; PRT; 9 AA.
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas l.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
ON NCBI_TaxID=6759;
RN [1]
RP SEQUENCE
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 927 MW; 832D79CDBC46D861 CRC64;
Query Match 2.5%; Score 27; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 72 ATGKGF 79
| | | | |
DB 1 ATGQVAF 8

RESULT 13
CONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH)
DE (luliberin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Squalidae; Squalidae;
ON NCBI_TaxID=7797;
RN [1]
RP SEQUENCE
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
RT dogfish brain provides insight into GnRH evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A46030; A46030.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;
Query Match 2.5%; Score 27; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGNV 130
| | | | |
DB 1 QHWSHOWL 8
RESULT 14
CRBL_VESMA STANDARD; PRT; 13 AA.
AC P17232;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide M (VESCP-M).
OS Vespa mandarinia (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
ON NCBI_TaxID=7446;
RN [1]
RP SEQUENCE
RC TISSUE=Venom;
RX Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,
RA Fujino M.;
RL (In) Munekata E. (eds.);
RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,
RL Osaka (1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;
Query Match 2.5%; Score 27; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 160 VFGKVLGEM 168
: ||| |
Db 4 IIGKVLGSL 12

RESULT 15
CREL_VESTR STANDARD; PRT; 13 AA.
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide T (VesCP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7450;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Yasuhara T., Nakajima T., Erspaer V.;
RL (In) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 2.5%; Score 27; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 160 VFGKVLGEM 168
: ||| |
Db 4 IIGKVLGSL 12

RESULT 16
TEMP_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RA "Temporins, antimicrobial peptides from the European red frog Rana
RL temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-negative and
Gram-positive bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9D8CC338 CRC64;

Query Match 2.5%; Score 27; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 160 VFGKVLGEM 168
: ||| |
Db 4 IIGKVLGSL 12

RESULT 17
TKN_KASSE STANDARD; PRT; 12 AA.
AC P08611;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A., Montecucchi P.C., Erspaer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
RT dodecapeptide from the skin of the African frog Kassina
RT senegalensis."
RL Experientia 33:857-858(1977).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07206; S07206.
DR PDB; 1MWU; 16-OCT-02.
DR InterPro; IPR002040; Tachy Neurokinin.
DR Pfam; PF02202; Tachykinin_1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW 3D-structure.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match 2.4%; Score 26.5; DB 1; Length 12;
Best Local Similarity 63.6%; Pred. No. 1.1e+04;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 61 VPRTVDNFVAL 71
: ||| |
Db 2 VPKS-DQFVGL 11

RESULT 18
GON2_CHICK STANDARD; PRT; 10 AA.
AC P37043; P20408; P81750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GnRH-II)
DE (LH-RH II) (Luliberin II).
OS Gallus gallus (Chicken).
OS Alligator mississippiensis (American alligator),
OS Squalus acanthias (Spiny dogfish),
OS Hydrolagus colliei (Spotted ratfish), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 8496, 7797, 7873, 30724;

```

```

RN RP SEQUENCE.
RC SPECIES=Chicken; TISSUE=Hypothalamus;
RX MEDLINE=84222059; PubMed=6427779;
RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA Matsuo H.;
RT "Identification of the second gonadotropin-releasing hormone in
RT chicken hypothalamus: evidence that gonadotropin secretion is
RT probably controlled by two distinct gonadotropin-releasing hormones
RT in avian species.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN [2]
RN SEQUENCE.
RC SPECIES=A. mississippiensis; TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
RN [3]
RN SEQUENCE.
RC SPECIES=S. acanthias; TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
RT dogfish brain provides insight into GnRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
RN [4]
RN SEQUENCE.
RC SPECIES=H. colliei; TISSUE=Brain;
RX MEDLINE=91340067; PubMed=1678723;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA Lee T.;
RT "Primary structure of gonadotropin-releasing hormone from the brain
RT of a holoccephalan (ratfish: Hydrolagus colliei).";
RL Gen. Comp. Endocrinol. 82:152-161(1991).
RN [5]
RN SEQUENCE, AND FUNCTION.
RC SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
RN CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC PIR; A61126; A61126.
DR PIR; A61126; A61126.
DR PIR; B46030; B46030.
DR PIR; B60066; B60066.
DR InterPro: IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;

Query Match 2.4%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 129
DB 1 QHWSHGW 7

RESULT 19
GON3 ONCKE STANDARD; PRT; 10 AA.
ID _GON3_ONCKE

```

```

AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
RH III) (Luliberin III).
GN GNRH3.
OS Oncorhynchus keta (Chum salmon), and
OS Clupea pallasi (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 30724;
RN [1]
RN SEQUENCE.
RC SPECIES=O. keta; PubMed=6341999;
RX MEDLINE=83195140; PubMed=10650929;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RN SEQUENCE, AND FUNCTION.
RC SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
RN CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A21114; A21114.
DR InterPro: IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 2.4%; Score 26; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 1e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 130
DB 1 QHWSYGL 8

RESULT 20
FIF1 SARBU STANDARD; PRT; 12 AA.
ID FIF1 SARBU
AC P83349.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RN SEQUENCE, AMIDATION, AND FUNCTION.
RP SEQUENCE-CNS;
RC TISSUE-CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
 Query Match 2.4%; Score 26; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 62 PKTVDFNV 69
 : : : : :
 Db 3 FQPSDNFI 10
 RESULT 21
 ID TEMA RANTE STANDARD; PRT; 13 AA.
 AC P56917;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Temporin A.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 CC NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the brevinin family.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD RES 13 13 AMIDATION
 SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;
 Query Match 2.4%; Score 26; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 49 VGRVIFGL 56
 : : : : :
 Db 5 IGRVLSGI 12
 RESULT 22
 ID CRBL VESOR STANDARD; PRT; 14 AA.
 AC P17236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histamine releasing peptide II (HR-II).
 OS Vespa orientalis (Oriental hornet).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 CC Vespidae; Vespinae; Vespa.
 CC NCBI_TaxID=7447;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Venom;
 RA Miroshnikov A.I., Snehkova L.G., Nazimov I.V., Reshetova O.I.,
 RA Rozynov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 RT venom of Vespa orientalis hornet.";
 RL Bioorg. Khim. 7:1467-1477(1981).
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 CC of neutrophils.
 CC PIR: JN0390; JN0390.
 DR Mast cell degranulation; Chemotaxis; Amidation.
 KW MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1524 MW; 22015BA46CEDFD38 CRC64;
 Query Match 2.4%; Score 26; DB 1; Length 14;
 Best Local Similarity 30.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 159 VFVGKVLGM 168
 : : : : :
 Db 4 LILGLVKGL 13
 RESULT 23
 ID FIBB MANLE STANDARD; PRT; 14 AA.
 AC P14474;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Mandrillus.
 CC NCBI_TaxID=9568;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69115139; PubMed=4974768;
 RA Doolittle R.F., Glasgow C., Moss G.A.;
 RT "Characterization of fibrinopeptides A and B from a drill (Mandrillus
 RT leucophaeus).";
 RL Biochim. Biophys. Acta 175:217-219(1969).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 DR Interpro: IPR002181; Fibrinogen C.
 DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Pyrrolidone carboxylic acid.
 FT PEPTIDE 1 14 FIBRINOPEPTIDE B.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER -4 14
 SQ SEQUENCE 14 AA; 1434 MW; 6695B0F1EF72E1B CRC64;
 Query Match 2.4%; Score 26; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 1.5e+04;
 Matches 6; Conservative 2; Mismatches 0; Indels 6; Gaps 1;
 QY 45 GDEDVGRVIFGLFG 58
 : : : : :
 Db 5 GBEE-----GLFG 12
 RESULT 24
 ID AKH MELML STANDARD; PRT; 8 AA.
 AC P25423;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Melolontha melolontha (Cockchafer),
 OS Geotrupes stercorosus (Dor beetle), and
 OS Pachnoda marginata (Flower beetle).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
 OC Scarabaeidae; Melolonthinae; Melolontha.
 OC NCBI_TaxID=7061, 7087, 7058;
 RN [1]
 RN SEQUENCE.
 RP SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
 RC MEDLINE=91248100; PubMed=2039445;
 RX Gaede G.;
 RA "A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RT sequenced from two beetle species.";
 RL Biochem. J. 275:671-677(1991).
 RN [2]
 RN SEQUENCE.
 RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetonid beetle species determined by
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTX / RPCH family.
 CC A58641; A58641.
 DR PIR; S15422; S15422.
 DR PIR; S21663; S21663.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;
 QY 124 HYGPBW 129
 DB : |||
 DB 3 NYSPDW 8
 Query Match 2.3%; Score 25; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 124 HYGPBW 129
 DB : |||
 DB 3 NYSPDW 8
 RESULT 25
 AKH_TABAT
 ID AKH_TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH)
 DE (DCC 1).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Corpora cardiaca;
 RC MEDLINE=90046758; PubMed=2813385;
 RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: Hypotrehalosemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTX / RPCH family.
 CC PIR; B33995; B33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8
 Query Match 2.3%; Score 25; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTX / RPCH family.
 CC PIR; A33995; A33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8
 Query Match 2.3%; Score 25; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8
 RESULT 26
 HTF_TABAT
 ID HTF_TABAT STANDARD; PRT; 10 AA.
 AC P14596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypotrehalosemic factor (HOTH) (Dipteran corpora cardiaca factor II)
 DE (DCC II).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Corpora cardiaca;
 RC MEDLINE=90046758; PubMed=2813385;
 RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: Hypotrehalosemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph (trehalose is the
 CC major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTX / RPCH family.
 CC PIR; B33995; B33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8
 Query Match 2.3%; Score 25; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 125 YGPBW 129
 DB : |||
 DB 4 FTGPBW 8

```

RESULT 27
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckevich M.D.; Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 2.3%; Score 25; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 112 GERRPD 117
|:|:|
Db 2 GKTFFD 7

RESULT 28
RS30 ONCMY
ID RS30 ONCMY STANDARD; PRT; 11 AA.
AC P83328;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
OS FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus; AND MASS SPECTROMETRY.
RX MEDLINE=22142142; PubMed=12147245;
RA Fernandes J.M.O.; Smith V.J.;
RT "A novel antimicrobial function for a ribosomal peptide from rainbow
trout skin.";
OS Biochem. Biophys. Res. Commun. 296:167-171(2002).
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON TER 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 2.3%; Score 25; DB 1; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 131 SWANAGK 137

```

```

Db 5 SLARAGK 11
|:|:|

RESULT 29
HS9A RAT
ID HS9A RAT STANDARD; PRT; 12 AA.
AC P82935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T.; Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
beta isoforms from rat liver.";
RL Proteoloma 218:54-56(2001).
CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the heat shock protein 90 family.
DR InterPro; IPR001404; Hsp90.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 12 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 2.3%; Score 25; DB 1; Length 12;
Best Local Similarity 30.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 178 KTDSDKDKLK 187
|:|:|:|:|
Db 3 ETQTQDQPM 12

RESULT 30
TA13 TREME
ID TA13 TREME STANDARD; PRT; 13 AA.
AC P01370;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tremorgen A-13.
OS Tremella mesenterica (Jelly fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
OX NCBI_TaxID=5217;
RN [1]
RP SEQUENCE.
RA Sakagami Y.; Yoshida M.; Isogai A.; Suzuki A.;
RT "Peptide sex hormones inducing conjugation tube formation in
compatible mating-type cells of Tremella mesenterica.";
RL Science 212:1525-1527(1981).
CC -!- FUNCTION: Tremorgen A-13 is produced by the a mating-type cells
and induces formation of conjugation tubes in a mating-type cells.
CC PIR; A01641; JTG03.
KW Lipoprotein; Prenylation; Pheromone.
FT LIPID 13 13
SQ SEQUENCE 13 AA; 1204 MW; 6803049697BA864 CRC64;

```

Query Match 2.3%; Score 24.5; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 95 QGGDFTRGDGTG 106
DB 1 EGGG-NRGDPFG 11

RESULT 31
BRK ONCMY
ID BRK ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma."
RL PDB Lett. 334:75-78 (1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the bradykinin family.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 2.2%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 127 PGW 129
DB 4 PGW 6

RESULT 32
CAER LITXA
ID CAER LITXA STANDARD; PRT; 10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein.
OS Litoria xanthomera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J., Ramsay S.L.;
RT "New caerin antipeptide peptides from the skin glands of the Australian tree frog Litoria xanthomera."
RL J. Pept. Sci. 3:181-185 (1997).
CC -1- FUNCTION: Hypotensive neuro-peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.

CC -1- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 4 4 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DEF3837861BB5A CRC64;

Query Match 2.2%; Score 24; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 151 TAWLD 155
DB 5 TGMWD 9

RESULT 33
TKS1 AEDAE
ID TKS1 AEDAE STANDARD; PRT; 10 AA.
AC P42634;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokinin I.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RX STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aedes aegypti."
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142 (1994).
CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the site of feeding.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A49581; A49581.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; 3DCFDE6B59C33AA8 CRC64;

Query Match 2.2%; Score 24; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 73 TGEKGF 79
DB 2 TGDKFY 8

RESULT 34
TKS2 AEDAE
ID TKS2 AEDAE STANDARD; PRT; 10 AA.
AC P42635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]

```
RP SEQUENCE.
RC STRAIN-Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT mosquito Aedes aegypti.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC site of feeding.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; B49581; B49581.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 2.2%; Score 24; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 73 TGEKGFQ 79
DB 2 TGDKFYG 8

RESULT 35
HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Blaise D., Severini C., Alta M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 2.2%; Score 24; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 52 VIFGLFGK 59
DB 4 LIAGLLGK 11

RESULT 36
RFL CONSP STANDARD; PRT; 12 AA.
AC P58805;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

```
DE Conorfamide-Srl.
OS Conus spurius (Alphabet cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=192919;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21605839; PubMed=11738233;
RA Maillio M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA Olivera B.M., Heimer de la Coteria E.P.;
RT "Conorfamide, a Conus venom peptide belonging to the Rfamidae family of
RT neuropeptides.";
RL Toxicon 40:401-407(2002).
CC -!- FUNCTION: Causes hyperactivity in mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neurotoxin; Toxin; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;

Query Match 2.2%; Score 23.5; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 126 GP-GWV 130
DB 1 GPMGWV 6

RESULT 37
UN46 CLOPA STANDARD; PRT; 14 AA.
ID UN46 CLOPA STANDARD; PRT; 14 AA.
AC P81362;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein Cp 46 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 38.2 kDa.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1550 MW; 198078F4C0367170 CRC64;

Query Match 2.2%; Score 23.5; DB 1; Length 14;
Best Local Similarity 38.5%; Pred. No. 2.4e+04;
Matches 5; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 38 VVFDLRIGDEDVG 50
DB 2 IFNDL-IGNNNIG 13

RESULT 38
LMT2 LOCM1 STANDARD; PRT; 8 AA.
ID LMT2 LOCM1 STANDARD; PRT; 8 AA.
AC P22396;
DT 01-AUG-1991 (Rel. 19, Created)
```

```

DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Locustamyototropin 2 (LOM-MT-2)
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyototropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotrophic peptide family."
RL Insect Biochem. 20:479-484 (1990).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8 AMIDATION.
FT SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;
SQ
Query Match 2.1%; Score 23; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 GDFT 100
Db |||||
2 GDFT 5

RESULT 39
COXO RAT
ID _COXO RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE (VIIIA) (Fragment).
DE COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241 (1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S65388; S65388.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;
SQ
Query Match 2.1%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 124 HY--GPG 128
Db |||||
2 HYAEGPG 8

```

```

Db |||||
2 HYEFGPG 8

RESULT 40
COXO THUOB
ID _COXO THUOB STANDARD; PRT; 10 AA.
AC P80952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103 (1997).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S77990; S77990.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;
SQ
Query Match 2.1%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 124 HY--GPG 128
Db |||||
2 HYEFGPG 8

RESULT 41
URA7 HUMAN
ID _URA7 HUMAN STANDARD; PRT; 10 AA.
AC P34990;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Erythrocyte;
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RL Submitted (FEB-1994) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.77, its MW is: 26 kDa.
DR SWISS-2DPAGE; P34990; HUMAN.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;
SQ

```

Query Match 2.1%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.9e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 111 YGPRPD 117
 :|||
 Db 3 HGENFXD 9

RESULT 42
 ID CORZ_PERAM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Venstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from
 the American cockroach.";
 RL FEBS Lett. 250:231-234 (1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR: S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 2.1%; Score 23; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 2e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 125 YGPGWVS 131
 :|||
 Db 5 YSRGWTN 11

RESULT 43
 ID TKN4_PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SPI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304 (1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and

secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Balongs to the tachykinin family.
 DR PIR: E60409; E60409.
 DR InterPro: IPR002040; TachyNeurokinin.
 DR InterPro: IPR008215; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CBIAB7 CRC64;

Query Match 2.1%; Score 23; DB 1; Length 11;
 Best Local Similarity 71.4%; Pred. No. 2e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 116 PDENFKL 122
 :|||
 Db 4 PDEFFGL 10

RESULT 44
 ID ADFB_TENMO STANDARD; PRT; 13 AA.
 AC P83109;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Antidiuretic factor B (ADFB).
 OS Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
 RP SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=22465067; PubMed=12576082;
 RA Eigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
 Hull J.J., Schooley D.A.;
 RT "Isolation, identification and localization of a second beetle
 antidiuretic peptide.";
 RL Peptides 24:27-34 (2003).
 CC -!- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
 CGMP as second messenger. May function as an antidiuretic
 hormone.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
 pairs of bilaterally symmetrical cells in the protocerebrum.
 CC -!- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI.
 KW Neuropeptide; Hormone.
 SQ SEQUENCE 13 AA; 1562 MW; 0240A4504BA632B CRC64;

Query Match 2.1%; Score 23; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 103 DGTGKSIYG 112
 :|||
 Db 3 DGSYKPHIYG 12

RESULT 45
 ID MAST_VESCR STANDARD; PRT; 14 AA.
 AC P01516;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan C.
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=84289390; PubMed=6206053;
RA Argiolas A., Pisano J.J.;
RT "Isolation and characterization of two new peptides, mastoparan C and
RL crabrolin, from the venom of the European hornet, Vespa crabro.";
RL J. Biol. Chem. 259:10106-10111(1984).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; A01779; QWHP2.
KW Mast cell degranulation; Amidation.
FT MOD RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1508 MW; 550C0ECALD6AB1D7 CRC64;

Query Match 2.1%; Score 23; DB 1; Length 14;
Best Local Similarity 62.5%; Pred.No; 2.6e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVLLAAA 8
Db :||| |
3 LKALLAVA 10

Search completed: August 30, 2004, 10:50:26
Job time : 36.8378 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 62.5405 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAALIAAGSVFFLLP.....VIIADCGKIEVXPFAAKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:**

1: Pir1:**
2: Pir2:**
3: Pir3:**
4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	2.9	11	2	PT0218
2	31	2.9	13	2	PH0796
3	30	2.8	13	2	JQ1350
4	29	2.7	8	2	PT0279
5	29	2.7	8	2	PT0725
6	29	2.7	8	2	PT0588
7	29	2.7	12	2	G49410
8	28	2.6	8	2	A61348
9	28	2.6	10	2	A50421
10	28	2.6	10	2	S08997
11	28	2.6	10	2	S08998
12	28	2.6	10	2	A26381
13	28	2.6	11	2	S57575
14	28	2.6	12	2	PH1458
15	28	2.6	13	2	S78766
16	27.5	2.5	13	2	B56864
17	27	2.5	10	2	A46030
18	27	2.5	11	2	B60769
19	27	2.5	14	2	PA0096
20	27	2.5	14	2	PH0801
21	26.5	2.4	12	2	S07206
22	26.5	2.4	13	2	A23695
23	26.5	2.4	14	2	S33802
24	26.5	2.4	14	2	PH0747
25	26	2.4	8	2	S55310
26	26	2.4	8	2	A58620
27	26	2.4	8	2	PT0554
28	26	2.4	9	2	PT0231
29	26	2.4	10	1	RHAQ2

```

30      26      2.4      10      1      A61126      gonadoliberin - sp
31      26      2.4      10      2      B46030      gonadoliberin II -
32      26      2.4      10      2      A21114      gonadoliberin - ch
33      26      2.4      11      2      C38887      T-cell receptor ga
34      26      2.4      12      2      S26544      hemoglobin, extrac
35      26      2.4      12      2      S65730      Ig kappa-1 chain J
36      26      2.4      13      2      C53275      histamine-releasin
37      26      2.4      14      2      JN0390      T-cell receptor al
38      26      2.4      14      2      PH0795      adipokinetic hormo
39      25      2.3      8      2      S15422      adipokinetic hormo
40      25      2.3      8      2      A33995      adipokinetic hormo
41      25      2.3      8      2      A58641      neuropeptide - flo
42      25      2.3      8      2      S21663      T-cell receptor be
43      25      2.3      8      2      PT0595      hypotrehalosemic h
44      25      2.3      10      2      B33995      S-layer protein -
45      25      2.3      10      2      A60476

```

ALIGNMENTS

RESULT 1

PT0218
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0218
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0218

A:Molecule type: mRNA

A:Residues: 1-11 <NAK>

C:Keywords: T-cell receptor

Query Match 2.9%; Score 31; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 102 GDGTGKSIY 111

Db 2 GAGGGNTLY 11

RESULT 2

PH0796
T-cell receptor alpha chain (F15) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0796

R:Caanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r alleles exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0796

A:Molecule type: mRNA

A:Residues: 1-13 <CAS>

A:Cross-references: EMBL:X60901

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 2.9%; Score 31; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 9.6e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 102 GDGTGKSIY 112

Db 3 GTGNTGLIFG 13

RESULT 3

JQ1350
 hypothetical protein, 1.3K (rps16 5' region) - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
 C:Accession: JQ1350
 R:Bradshaw, R.E.; Pillar, T.M.
 Gene 108, 157-162, 1991
 A:Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gene from *Emericella nidulans*
 A:Reference number: JQ1349; MUID:92104500; PMID:1761226
 A:Accession: JQ1350
 A:Molecule type: DNA
 A:Residues: 1-13 <BRA>
 A:Cross-references: GB:M65259; NID:gi68087; PID:gi68089
 A:Experimental source: strain R153

Query Match 2.8%; Score 30; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 67 NFVALATGK 76
 ||| |||
 DB 2 NMVCAATGK 11

RESULT 4
 PT0279
 IG heavy chain CRD3 region (clone 4-91A) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0279
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J_H gene segments in the development of the human IgG1 heavy chain
 A:Reference number: PT0222; MUID:91108337; PMID:1999102
 A:Accession: PT0279
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 2.7%; Score 29; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 102 GDGTGG 107
 ||| |||
 DB 3 GDGRGG 8

RESULT 5
 PT0725
 T-cell receptor beta chain V-D-J region (140-21) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0725
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0725
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-8 <FEE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 2.7%; Score 29; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 102 GDGTGG 107
 ||| |||
 DB 3 GDGLGG 8

RESULT 6
 PT0588
 T-cell receptor beta chain V-D-J region (141-1CB) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0588
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0588
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 2.7%; Score 29; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.8e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 102 GDGTGG 107
 ||| |||
 DB 3 GDATGG 8

RESULT 7
 G49410
 t-complex polypeptide 1 homolog (peak 6b fraction) - rabbit (fragment)
 N:Alternate names: chaperonin homolog (peak 6b)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 04-Sep-1998
 C:Accession: G49410
 R:Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Am
 Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
 A:Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela
 A:Reference number: A49410; MUID:94089752; PMID:7903455
 A:Accession: G49410
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <ROM>
 A:Experimental source: reticulocyte
 C:Superfamily: molecular chaperone t-complex-type

Query Match 2.7%; Score 29; DB 2; Length 12;
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 130 VSMANAGKDTN 140
 : : : : :
 DB 1 ILIANTGMDTD 11

RESULT 8
 A61348
 red pigment-concentrating hormone - northern shrimp
 N:Alternate names: blanching hormone
 C:Species: Pandalus borealis (northern shrimp)
 C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C:Accession: A61348; S07139
 R:Fernlund, P.; Josefsson, L.
 Science 177, 173-175, 1972
 A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
 A:Reference number: A61348; MUID:72228738; PMID:5041353
 A:Accession: A61348
 A:Molecule type: protein
 A:Residues: 1-8 <FER1>
 R:Fernlund, P.
 Biochim. Biophys. Acta 371, 304-311, 1974
 A:Title: Structure of the red-pigment-concentrating hormone of the shrimp, *Pandalus borealis*
 A:Reference number: S07139; MUID:75054965; PMID:4433559

A;Accession: S07139
A;Molecule type: protein
A;Residues: 'E', 2-8 <FER2>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
zed pigment-containing cells.
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129
:: |||
Db 3 NFSPGW 8

RESULT 9
A60421
hypertrehalosemic hormone - German cockroach
N;Alternate names: Bld-HrTH
C;Species: Blattella germanica (German cockroach)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997
C;Accession: A60421; S09137
R;Veenstra, J.A.; Camps, F.
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Biatte
Neuropeptides 15, 107-109, 1990
A;Reference number: A60421; MUID:91179584; PMID:2080017
A;Accession: A60421
A;Molecule type: protein
A;Residues: 1-10 <VE>
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09137
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 1; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129
:: |||
Db 3 NFSPGW 8

RESULT 10
S08997
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08997
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 1; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129

:: |||

Db 3 NFSPGW 8

RESULT 11

S08998

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997

C;Accession: S08998

R;Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998

A;Molecule type: protein

A;Residues: 1-10 <GAE>

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.3e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129

:: |||

Db 3 NFSPGW 8

RESULT 12

A26381

hypertrehalosemic hormone - gray cockroach

C;Species: Nauphoeta cinerea (gray cockroach)

C;Date: 31-Mar-1988 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997

C;Accession: A26381

R;Gaede, G.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 141, 774-781, 1986

A;Title: Amino acid sequence of a hypertrehalosemic neuropeptide from the corpus cardiac
A;Reference number: A26381; MUID:87100208; PMID:3801028

A;Accession: A26381

A;Molecule type: protein

A;Residues: 1-10 <GAD>

A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 2.6%; Score 28; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 1.3e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129

:: |||

Db 3 NFSPGW 8

RESULT 13

S57575

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57575

R.; Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A: Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A: Reference number: S57494
A: Accession: S57575
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-11 <BUR>
A: Cross-references: EMBL:Z49953; NID:G887510; PIDN:CAA90224.1; PID:G887511
C: Keywords: T-cell receptor

Query Match 2.6%; Score 28; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 106 GKGSIYG 112
DB 5 GGLKIFG 11

RESULT 14
PH1458
T-cell receptor beta chain (clone 332/1K) - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
C: Accession: PH1458; S26543
R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A: Title: T cell receptor selection by and recognition of two class I major histocompatib
A: Reference number: PH1430; MUID:93171821; PMID:8436911
A: Accession: PH1458
A: Molecule type: mRNA
A: Residues: 1-12 <CAS>
A: Experimental source: cytolytic T-lymphocyte, clone 332/1K
R: Casanova, J.L.; Carottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A: Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A: Reference number: S26512; MUID:92364546; PMID:1380061
A: Accession: S26543
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-12 <CA2>
A: Cross-references: EMBL:X67993
A: Experimental source: cytolytic T-lymphocyte, clone Cw3/C44
C: Superfamily: immunoglobulin homology
C: Keywords: receptor; T-cell

Query Match 2.6%; Score 28; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 95 QGGDFTRG 102
DB 5 QGSDYTFG 12

RESULT 15
S78766
ribosomal protein MRP-S28, mitochondrial - bovine (fragment)
C: Species: Bos primigenius taurus (cattle)
C: Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C: Accession: S78766
R: Grack, H.R.
submitted to the Protein Sequence Database, July 1999
A: Reference number: S78760
A: Accession: S78766
A: Molecule type: protein
A: Residues: 1-13 <GRA>
C: Keywords: mitochondrion
F: 1-13/Product: ribosomal protein MRP-S28 (fragment) #status experimental <MAT>

Query Match 2.6%; Score 28; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.7e+04;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 62 PKTVNFFVAL 71
DB 3 PKNVESFASM 12

RESULT 16
B56864
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C: Species: Bos primigenius taurus (cattle)
C: Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C: Accession: B56864
R: Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993
A: Title: The oligomeric structure of renal
A: Reference number: A56864; MUID:93136203; PMID:8093665
A: Accession: B56864
A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-13 <PLA>
A: Experimental source: renal brush-border membrane vesicles
C: Keywords: dipeptidylpeptidase hydrolase

Query Match 2.5%; Score 27.5; DB 2; Length 13;
Best Local Similarity 35.0%; Pred. No. 1.9e+04;
Matches 7; Conservative 2; Mismatches 2; Indels 9; Gaps 1;

QY 149 VKTAMLDGKHVFGKVLGQM 168
DB 1 MKTPW-----KVLGSL 11

RESULT 17
A46030
gonadoliberin I - spiny dogfish
N: Alternate names: gonadotropin-releasing hormone
C: Species: Squalus acanthias (spiny dogfish)
C: Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Dec-1998
C: Accession: A46030
R: Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A: Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro
A: Reference number: A46030; MUID:92335300; PMID:1631133
A: Accession: A46030
A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-10 <LOV>
C: Keywords: hormone; pyroglutamic acid
F: 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 2.5%; Score 27; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.6e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGWV 130
DB 1 QHWSHGWL 8

RESULT 18
B60769
IG H2 chain - Pacific hagfish (fragment)
C: Species: Eptatretus stouti (Pacific hagfish)
C: Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C: Accession: B60769
R: Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A: Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A: Reference number: A60769; MUID:91060965; PMID:2123225
A: Accession: B60769
A: Status: preliminary
A: Molecule type: protein

A;Residues: 1-11 <HAN>

Query Match 2.5%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 90 KDFMIQ 95

Db 4 EDFMIQ 9

RESULT 19

PA0096

pyruvate decarboxylase (EC 4.1.1.1) 1 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0096

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PA0051

A;Accession: PA0096

A;Molecule type: protein

A;Residues: 1-14 <CHO>

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 2.5%; Score 27; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 36 VKVYFDLRIGDE 47

Db 1 VXAYFDGLPGDQ 12

RESULT 20

PH0801

T-cell receptor alpha chain (J5) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0801

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-x-linked

allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0801

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60909

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 2.5%; Score 27; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.2e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 104 GTGKSIYV 112

Db 6 GTGKSLSPG 14

RESULT 21

S07206

kassinin - Senegal running frog

C;Species: Kassina senegalensis (Senegal running frog)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000

C;Accession: S07206

R;Anastasi, A.; Montecucchi, P.; Erspamer, V.; Vissier, J.

Experientia 33, 857-858, 1977

A;Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from

A;Reference number: S07206; MUID:77246385; PMID:891753

A;Accession: S07206

A;Molecule type: protein

A;Residues: 1-12 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end

F;12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 2.4%; Score 26.5; DB 2; Length 12;

Best Local Similarity 63.6%; Pred. No. 2.1e+04;

Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 61 VPKTVDNFVAL 71

Db 2 VPXS-DQFVGL 11

RESULT 22

A23695

myosin heavy chain, smooth muscle - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 02-Feb-2001

C;Accession: A23695

R;Garabedian, T.E.; Yount, R.G.

J. Biol. Chem. 265, 22547-22553, 1990

A;Title: Direct photoaffinity labeling of gizzard myosin with [3H]uridine diphosphate plus

A;Reference number: A23695; MUID:91093106; PMID:1979981

A;Accession: A23695

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <GAR>

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: nucleotide binding; P-loop; smooth muscle

F;2-9/Region: nucleotide-binding motif A (P-loop)

Query Match 2.4%; Score 26.5; DB 2; Length 13;

Best Local Similarity 53.8%; Pred. No. 2.3e+04;

Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 73 TGEKGFYKNSK 84

Db 1 TGESGAGKENTK 13

RESULT 23

S33802

chaperone, TCPI-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999

C;Accession: S33802

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Schaefer, A.A.; Schaefer, A.

Nature 363, 644-648, 1993

A;Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo-

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

Query Match 2.4%; Score 26.5; DB 2; Length 14;

Best Local Similarity 46.2%; Pred. No. 2.5e+04;

Matches 6; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 118 ENFKLKHVPGMW 130

Db 3 ESACL---GPWWI 12

RESULT 24

PH0747

T-cell receptor beta chain (M1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0747

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-II allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1836010
 A;Accession: PH0747
 A;Molecule type: mRNA
 A;Residues: 1-14 <CAS>
 A;Cross-references: EMBL:X60838
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match 2.4%; Score 26.5; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 2.5e+04;
 Matches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 104 GTGCKSIYGERP 115
 : : : : :
 Db 4 GTGG---FAEQF 12

RESULT 25
 S55310
 adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
 N;Alternate names: Psi-AKH
 C;Species: Pseudagrion inconspicuum
 C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: S55310
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994
 A>Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: S55310
 A;Molecule type: protein
 A;Residues: 1-8 <JAN>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129
 : : : : :
 Db 3 NFTPWG 8

RESULT 26
 A58620
 adipokinetic hormone - damselfly (Ischnura senegalensis)
 C;Species: Ischnura senegalensis
 C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
 C;Accession: A58620
 R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
 Biochem. J. 302, 539-543, 1994
 A>Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum
 A;Reference number: S55310; MUID:94379987; PMID:8093008
 A;Accession: A58620
 A;Molecule type: protein
 A;Residues: 1-8 <JAN>
 C;Superfamily: adipokinetic hormone
 C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 124 HYGPWG 129
 : : : : :
 Db 3 NFTPWG 8

RESULT 27

PT0554
 T-cell receptor beta chain V-D-J region (126-1G) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0554
 R;Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0554
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-8 <FEE>
 A;Experimental source: day 18 fetal thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 72 ATCEKGFG 79
 : : : : :
 Db 1 ASGDEGLG 8

RESULT 28
 PT0231
 IG heavy chain CDR3 region (clone 1-118) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0231
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:91108337; PMID:1899102
 A;Accession: PT0231
 A;Molecule type: DNA
 A;Residues: 1-9 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 2.4%; Score 26; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 125 YGPGWVS 131
 : : : : :
 Db 3 HSSGWVS 9

RESULT 29
 RHAQ2
 gonadoliberin II - American alligator
 N;Alternate names: gonadotropin-releasing hormone II
 C;Species: Alligator mississippiensis (American alligator)
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
 C;Accession: B60066
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
 Regul. Pept. 33, 105-116, 1991
 A>Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
 A;Reference number: A60066; MUID:91352338; PMID:1882082
 A;Accession: B60066
 A;Molecule type: protein
 A;Residues: 1-10 <LOV>
 C;Superfamily: Gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 2.4%; Score 26; DB 1; Length 10;

Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 129
:|: ||
Db 1 QHWSHG 7

RESULT 30
A61126
gonadoliberin - spotted ratfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Hydrolagus colliei (spotted ratfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 18-Mar-1997
C;Accession: A61126
R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
Gen. Comp. Endocrinol. 82, 152-161, 1991
A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocope
A;Reference number: A61126; MUID:91340067; PMID:1678723
A;Accession: A61126
A;Molecule type: protein
A;Residues: 1-10 <LOV>
A;Experimental source: brain
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F;1/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 2.4%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 129
:|: ||
Db 1 QHWSHG 7

RESULT 31
B46030
gonadoliberin II - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jan-2003
C;Accession: B46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: B46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 129
:|: ||
Db 1 QHWSHG 7

RESULT 32
A21114
gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 19-Jun-1993
C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.
Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 129
:|: ||
Db 1 QHWSHG 7

RESULT 33
A21114
gonadoliberin - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

Best Local Similarity 42.9%; Pred. No. 1.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 130
:|: ||
Db 1 QHWSYGL 8

Query Match 2.4%; Score 26; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 34
C38887
T-cell receptor gamma chain (5a.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+04;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 135 AGKDTNG 141
||: ||
Db 4 AGRDSSG 10

RESULT 35
S26544
T-cell receptor beta chain (clone Cw3/HLA1C8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26544
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptors
A;Reference number: S26542; MUID:92364546; PMID:1380061
A;Accession: S26544
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67994
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1C8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 95 QGDFPTRG 102
||: ||
Db 5 QGTDYTFG 12

RESULT 35
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

A;Title: Characterization of a teleost gonadotropin-releasing hormone.
A;Reference number: A21114; MUID:83195140; PMID:6341999
A;Accession: A21114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>

Query Match 2.4%; Score 26; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.9e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 123 KHYGPGW 130
:|: ||
Db 1 QHWSYGL 8

RESULT 33
C38887
T-cell receptor gamma chain (5a.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C38887
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C38887
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.1e+04;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 135 AGKDTNG 141
||: ||
Db 4 AGRDSSG 10

RESULT 34
S26544
T-cell receptor beta chain (clone Cw3/HLA1C8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26544
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptors
A;Reference number: S26542; MUID:92364546; PMID:1380061
A;Accession: S26544
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X67994
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1C8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 2.4%; Score 26; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 95 QGDFPTRG 102
||: ||
Db 5 QGTDYTFG 12

RESULT 35
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

RESULT 37

JN0390
histamine-releasing peptide II - oriental hornet
N; Alternate names: venom protein HR-2
C; Species: Vespa orientalis (oriental hornet)
C; Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 23-Aug-1997
C; Accession: JN0390; S10919
R; R; Mirosnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus
Bioorg. Khim. 7, 1467-1477, 1981
A; Title: Structure and properties of histamine releasing peptides from the venom of Vespa
A; Reference number: JN0389
A; Accession: JN0390
A; Molecule type: protein
A; Residues: 1-14 <MIR>
R; Tuichibaev, N.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A; Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St
A; Reference number: S06445
A; Accession: S10919
A; Molecule type: protein
A; Residues: 1-14 <TUR>
C; Superfamily: crabrolin
C; Keywords: amidated carboxyl end; venom
F; 14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 2.4%; Score 26; DB 2; Length 14;
Best Local Similarity 30.0%; Pred. No. 2.7e+04;

A;Residues: 1-8 <JAF>
C;Superfamily: adipokinetic hormone
F;1/Modified site: amidated carboxyl end (Gln) #status predicted
F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 125 YGPGW 129
Db 4 FTFGW 8

RESULT 41
A58641
adipokinetic hormone - dor beetle
C;Species: Geotrupes stercorosus (dor beetle)
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
C;Accession: A58641
R;Gaede, G.
Biochem. J. 275, 671-677, 1991
A;Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pigment concentrating hormone family
A;Reference number: S15422; MUID:91248100; PMID:2039445
A;Accession: A58641
A;Molecule type: protein
A;Residues: 1-8 <BIO>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuroptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
Db 3 NYSPDW 8

RESULT 42
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of various insects
A;Reference number: S21663; MUID:92265187; PMID:1586453
A;Accession: S21663
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 124 HYGPGW 129
Db 3 NYSPDW 8

RESULT 43
PT0595
T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0595

R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0595
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 2.3%; Score 25; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 103 DGTGG 107
Db 4 EGTGG 8

RESULT 44
B33995
hypotrehalosemic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: B33995
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuroptide hormones with adipokinetic and hypotrehalosemic activities
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuroptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 2.3%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 125 YGPGW 129
Db 4 FTFGW 8

RESULT 45
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C;Species: Bacillus thuringiensis
C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C;Accession: A60476
R;Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A;Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A;Reference number: A60476; MUID:90078111; PMID:2592346
A;Accession: A60476
A;Molecule type: protein
A;Residues: 1-10 <LUC>
C;Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 2.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 112 GERFPD 117
Db 2 GKTFPD 7

Search completed: August 30, 2004, 10:58:53
Job time : 62.5405 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 254.378 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 1083

Sequence: 1 MKVLLAALTAGSVFFLLP.....VIIADCGKIEVKEPFAIKE 208

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	7.7	14	15	US-10-394-980-52
2	54	5.0	14	12	US-10-014-340-347
3	50	4.6	9	16	US-10-447-161-85
4	50	4.6	9	16	US-10-788-016-2
5	49	4.5	9	16	US-10-447-161-84
6	49	4.5	9	16	US-10-788-016-1
7	47	4.3	9	16	US-10-788-016-9
8	36	3.3	11	10	US-09-972-656-7
9	36	3.3	13	9	US-09-873-637-9
10	36	3.3	13	13	US-09-876-904A-242
11	36	3.3	13	13	US-10-038-612-168
12	35	3.2	9	16	US-10-264-309-118
13	35	3.2	11	16	US-10-356-257-142
14	35	3.2	13	14	US-10-300-694A-66
15	35	3.2	14	12	US-10-247-839-101

16	34	3.1	9	12	US-09-988-493-293	Sequence 293, App
17	34	3.1	9	12	US-10-014-340-209	Sequence 209, App
18	34	3.1	11	12	US-09-995-388-8	Sequence 8, Appli
19	34	3.1	12	12	US-09-995-388-5	Sequence 5, Appli
20	34	3.1	12	14	US-10-193-477-146	Sequence 146, App
21	34	3.1	12	14	US-10-193-477-168	Sequence 168, App
22	32.5	3.0	13	14	US-10-017-193-8	Sequence 8, Appli
23	32	3.0	9	9	US-09-802-077-50	Sequence 50, Appli
24	32	3.0	9	9	US-09-802-096-50	Sequence 50, Appli
25	32	3.0	9	10	US-09-925-179-50	Sequence 27, Appli
26	32	3.0	9	14	US-10-223-172A-27	Sequence 27, Appli
27	32	3.0	9	14	US-10-224-999A-27	Sequence 17, Appli
28	32	3.0	10	9	US-09-802-077-17	Sequence 46, Appli
29	32	3.0	10	9	US-09-802-077-46	Sequence 17, Appli
30	32	3.0	10	9	US-09-802-096-17	Sequence 46, Appli
31	32	3.0	10	9	US-09-802-096-46	Sequence 17, Appli
32	32	3.0	10	10	US-09-925-179-17	Sequence 46, Appli
33	32	3.0	10	10	US-09-925-179-46	Sequence 33, Appli
34	32	3.0	10	10	US-09-755-630A-33	Sequence 33, Appli
35	32	3.0	10	14	US-10-223-172A-33	Sequence 33, Appli
36	32	3.0	10	14	US-10-224-999A-33	Sequence 33, Appli
37	32	3.0	11	12	US-09-995-388-9	Sequence 9, Appli
38	32	3.0	12	12	US-10-601-837-103	Sequence 103, App
39	32	3.0	12	14	US-10-224-999A-2922	Sequence 2922, Ap
40	32	3.0	13	10	US-09-991-225-19	Sequence 19, Appli
41	32	3.0	13	10	US-09-991-225-38	Sequence 38, Appli
42	32	3.0	13	12	US-10-369-405-19	Sequence 19, Appli
43	32	3.0	13	12	US-10-369-405-38	Sequence 38, Appli
44	32	3.0	13	14	US-10-224-999A-2931	Sequence 2931, Ap
45	32	3.0	13	14	US-10-224-999A-2932	Sequence 2932, Ap

ALIGNMENTS

RESULT 1

US-10-394-980-52
; Sequence 52, Application US/10394980
; Publication No. US20040005633A1
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: part of CYPB_HUMAN (peptidyl-prolyl cis-trans isomerase B)
US-10-394-980-52

Query Match 7.7%; Score 83; DB 15; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 HYGFGWYSMANAGK 137

DB 1 HYGFGWYSMANAGK 14

```
RESULT 2
US-10-014-340-347
; Sequence 347, Application US/10014340
; Publication No. US2003006441A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-347

Query Match          5.0%; Score 54; DB 12; Length 14;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 88 VIKDFMIQGGDFTR 101
Db 1 IIPGFMCGGGDFTR 14

RESULT 3
US-10-447-161-85
; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronection and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match          4.6%; Score 50; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
Db 1 DFMIQGGDF 9

RESULT 4
US-10-788-016-2
; Sequence 2, Application US/10798016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JPO2/08641
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
```

```
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
; OTHER INFORMATION: to the 99th residue of cyclophilin B
US-10-788-016-2

Query Match          4.6%; Score 50; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMIQGGDF 99
Db 1 DFMIQGGDF 9

RESULT 5
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronection and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match          4.5%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 KFHVRVIXDF 92
Db 1 KFHVRVIXDF 9

RESULT 6
US-10-788-016-1
; Sequence 1, Application US/10798016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JPO2/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
```

; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophilin B
US-10-788-016-1

Query Match 4.5%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 KHRVVKDF 92
Db 1 KHRVVKDF 9

RESULT 7
US-10-788-016-9
; Sequence 9, Application US/10788016
; Publication No. US2004014192A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
; OTHER INFORMATION: residues from the 91st residue to the 99th residue of
; OTHER INFORMATION: cyclophilin B
US-10-788-016-9

Query Match 4.3%; Score 47; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 91 DFMTQGGDF 99
Db 1 DYMTQGGDF 9

RESULT 8
US-09-972-656-7
; Sequence 7, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-7

Query Match 3.3%; Score 36; DB 10; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.3e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 102 GDTGGKSIY 111
Db 2 GDNLGKSLH 11

RESULT 9
US-09-873-637-9
; Sequence 9, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for SEQ ID NOS:3-8.
US-09-873-637-9

Query Match 3.3%; Score 36; DB 9; Length 13;
Best Local Similarity 63.6%; Pred. No. 4.2e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 97 GDFTRGDGTGG 107
Db 3 GGFGRGGGRGG 13

RESULT 10
US-09-876-904A-242
; Sequence 242, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 242
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: XPC gene product
US-09-876-904A-242

Query Match 3.3%; Score 36; DB 10; Length 13;
Best Local Similarity 58.8%; Pred. No. 4.2e+03;
Matches 10; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

Qy 21 GPSAADEKKKGKVTVK 37
Db 1 GPA----KKVAKVTVK 13

RESULT 11
US-10-038-612-168
; Sequence 168, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(13)
; OTHER INFORMATION: TrkB
US-10-038-612-168

Query Match 3.3%; Score 36; DB 13; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 119 NFKLKHYP 127
||||: |||
Db 3 NFKLRHGP 11

RESULT 12
US-10-264-309-118
; Sequence 118, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR.
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-118

Query Match 3.2%; Score 35; DB 16; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 115 FPDENFKLK 123
||||: |||
Db 1 FEDENFLK 9

RESULT 13
US-10-356-257-142
; Sequence 142, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 142
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-142

Query Match 3.2%; Score 35; DB 16; Length 11;
Best Local Similarity 77.8%; Pred. No. 4.3e+03;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 96 GGDFTRGDG 104
||||: |||
Db 2 GGDSTRGYG 10

RESULT 14
US-10-300-694A-66
; Sequence 66, Application US/10300694A
; Publication No. US20030185870A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Grinstead, Mark W.
; APPLICANT: Kenan, Daniel J.
; APPLICANT: Walsh, Elisabeth B.
; APPLICANT: Middleton, Crystan
; TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
; FILE REFERENCE: 180/143/2
; CURRENT APPLICATION NUMBER: US/10/300,694A
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/331,843
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Polycarbonate-binding peptide 66
US-10-300-694A-66

Query Match 3.2%; Score 35; DB 14; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.4e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 125 YPGWVSMNAG 136
:||||: |||
Db 1 FGHGWLTINLG 12

RESULT 15
US-10-247-839-101
; Sequence 101, Application US/10247839
; Publication No. US20040058400A1
; GENERAL INFORMATION:

APPLICANT: Holliger, Kaspar-Philipp
Griffiths, Andrew D
Hooenboom, Hendricus RJM
Malmqvist, Magnus
Marks, James D
McGuinness, Brian T
Pope, Anthony R
Prospero, Terence D
Winter, Gregory P
TITLE OF INVENTION: Multivalent and Multispecific Binding
Proteins, Their Manufacture and Use
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun
STREET: 6300 Sears Tower 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/247,839
FILING DATE: 20-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,979
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/448,418
FILING DATE: 14-MAY-1996
APPLICATION NUMBER: PCT/GB93/02492
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: GB 9300816.7
FILING DATE: 16-JAN-1993
APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32651
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide linker
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-247-839-101
Query Match 3.2%; Score 35; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 6e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 96 GGDFTRGDGTGKS 109
Db 1 GGGGGGGGGGGSS 14
RESULT 16
US-09-988-493-293
Sequence 293, Application US/09988493
Publication No. US2003006419A1
GENERAL INFORMATION:
APPLICANT: Herath, Mudiyansele Athula Chandrasiri
APPLICANT: O'Hare, Michael John
APPLICANT: Page, Martin John

APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Waterfield, Michael Derek
TITLE OF INVENTION: Proteins, Genes, and Their Use for Cancer
FILE REFERENCE: 2543-1-024
CURRENT APPLICATION NUMBER: US/09/988,493
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: PCT/GB01/01219
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0006695.1
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: GB 0007265.2
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 293
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapiens
US-09-988-493-293
Query Match 3.1%; Score 34; DB 12; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 115 FPDENFKLK 123
Db 1 FEDENFKLK 9
RESULT 17
US-10-014-340-209
Sequence 209, Application US/10014340
Publication No. US2003006411A1
GENERAL INFORMATION:
APPLICANT: Herath, et al
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
Diagnosis and Treatment of Alzheimer's Disease
FILE REFERENCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 209
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-340-209
Query Match 3.1%; Score 34; DB 12; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 115 FPDENFKLK 123
Db 1 FEDENFKLK 9
RESULT 18
US-09-995-388-8
Sequence 8, Application US/09995388
Publication No. US20020106325A1
GENERAL INFORMATION:
APPLICANT: Carpenter, Jr., Alan P.
TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITROECTIN
RECEPTOR TARGETED IMAGING AGENT
FILE REFERENCE: BMS-2201
CURRENT APPLICATION NUMBER: US/09/995,388
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 60/253,324
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.2

; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-995-388-8

Query Match 3.1%; Score 34; DB 12; Length 11;
Best Local Similarity 85.7%; Pred. No. 5.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
||| |||
Db 4 GDFKRGD 10

RESULT 19
US-09-995-388-5
; Sequence 5, Application US/09995388
; Publication No. US20020106325A1
; GENERAL INFORMATION:
; APPLICANT: Carpenter, Jr., Alan P.
; TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
; TITLE OF INVENTION: RECEPTOR TARGETED IMAGING AGENT
; FILE REFERENCE: BMS-2201
; CURRENT APPLICATION NUMBER: US/09/995,388
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/253,324
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-995-388-5

Query Match 3.1%; Score 34; DB 12; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
||| |||
Db 5 GDFKRGD 11

RESULT 20
US-10-193-477-146
; Sequence 146, Application US/10193477
; Publication No. US20030195163A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
; TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOGLOBULIN FOLDS, BGS2, 3, AND 4,
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0153 NP
; CURRENT APPLICATION NUMBER: US/10/193,477
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/304,888
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/372,147
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-477-146

Query Match 3.1%; Score 34; DB 14; Length 12;
Best Local Similarity 70.0%; Pred. No. 6.2e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 VFLLLPGPS 23
: || || || || |
Db 3 LFLLLPGPS 12

RESULT 21
US-10-193-477-168
; Sequence 168, Application US/10193477
; Publication No. US20030195163A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
; TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOGLOBULIN FOLDS, BGS2, 3, AND 4,
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0153 NP
; CURRENT APPLICATION NUMBER: US/10/193,477
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/304,888
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/372,147
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-477-168

Query Match 3.1%; Score 34; DB 14; Length 12;
Best Local Similarity 70.0%; Pred. No. 6.2e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 VFLLLPGPS 23
: || || || || |
Db 3 LFLLLPGPS 12

RESULT 22
US-10-017-193-8
; Sequence 8, Application US/10017193
; Publication No. US20030113478A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Mai Huong
; TITLE OF INVENTION: Surface Coating Method and Coated Device
; FILE REFERENCE: 52200-8010
; CURRENT APPLICATION NUMBER: US/10/017,193
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: attachment peptide from collagen
US-10-017-193-8

Query Match 3.0%; Score 32.5; DB 14; Length 13;
Best Local Similarity 70.0%; Pred. No. 1e+04;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 39 YFDLRI-GDE 47
||| ||| : |||
Db 4 YFDLRLKGD 13

RESULT 23

US-09-802-077-50
; Sequence 50, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-077-50

Query Match 3.0%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157
|||||
Db 4 WLDGK 8

RESULT 24
US-09-802-096-50
; Sequence 50, Application US/09802096
; Patent No. US20010033839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-096-50

Query Match 3.0%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157

Db 4 WLDGK 8
|||||
RESULT 25
US-09-925-179-50
; Sequence 50, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-925-179-50

Query Match 3.0%; Score 32; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157
|||||
Db 4 WLDGK 8

RESULT 26
US-10-223-172A-27
; Sequence 27, Application US/10223172A
; Publication No. US20030138444A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Zavitz, Kenton
; APPLICANT: Wettstein, Daniel Albert
; APPLICANT: Morham, Scott
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
; FILE REFERENCE: 5003.01
; CURRENT APPLICATION NUMBER: US/10/223,172A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/313,239
; PRIOR FILING DATE: 2001-08-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-223-172A-27

Query Match 3.0%; Score 32; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PGPSAADEX 28
|||||:
Db 1 PGPSAPPEE 9

RESULT 27

US-10-224-999A-27
; Sequence 27, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified HIV Peptide
US-10-224-999A-27

Query Match 3.0%; Score 32; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PGPSAADEX 28
|||||:
Db 1 PGPSAPPEE 9

RESULT 28

US-09-802-077-17
; Sequence 17, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-077-17

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||||

Db 5 WLDGK 9

RESULT 29

US-09-802-077-46
; Sequence 46, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-077-46

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||||

Db 5 WLDGK 9

RESULT 30

US-09-802-096-17
; Sequence 17, Application US/09802096
; Patent No. US20010033839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-096-17

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|
|
|
|
|
Db 5 WLDGK 9

RESULT 31
US-09-802-096-46
; Sequence 17, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-802-096-46

Query Match 3.0%; Score 32; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|
|
|
|
|
Db 5 WLDGK 9

RESULT 32
US-09-925-179-17
; Sequence 17, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1CIUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Artificial sequence

US-09-925-179-17

Query Match 3.0%; Score 32; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|
|
|
|
|
Db 5 WLDGK 9

RESULT 33
US-09-925-179-46
; Sequence 46, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1CIUS
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-09-925-179-46

Query Match 3.0%; Score 32; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|
|
|
|
|
Db 5 WLDGK 9

RESULT 34
US-09-755-630A-33
; Sequence 33, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
; APPLICANT: ALIBHALI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
; FILE REFERENCE: 11899.0217.NFUS00 (MOST217)
; CURRENT APPLICATION NUMBER: US/09/755,630A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence

FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-33

Query Match 3.0%; Score 32; DB 10; Length 10;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 201 KPFAIAKE 208
Db 3 RPFARAKE 10

RESULT 35
US-10-223-172A-33
Sequence 33, Application US/10223172A
Publication No. US2003013844A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Zavitz, Kenton
APPLICANT: Wettstein, Daniel Albert
APPLICANT: Morham, Scott
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
FILE REFERENCE: 5003.01
CURRENT APPLICATION NUMBER: US/10/223,172A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/313,239
PRIOR FILING DATE: 2001-08-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 10
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-223-172A-33

Query Match 3.0%; Score 32; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 8e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PGPSAADEK 28
Db 2 PGPSAPPEE 10

RESULT 36
US-10-224-999A-33
Sequence 33, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Modified HIV Peptide
US-10-224-999A-33

Query Match 3.0%; Score 32; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 8e+03;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 20 PGPSAADEK 28
Db 2 PGPSAPPEE 10

RESULT 37
US-09-995-388-9
Sequence 9, Application US/09995388
Publication No. US20020106325A1
GENERAL INFORMATION:
APPLICANT: Carpenter, Jr., Alan P.
TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
FILE REFERENCE: BMS-2201
CURRENT APPLICATION NUMBER: US/09/995,388
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 60/253,324
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-09-995-388-9

Query Match 3.0%; Score 32; DB 12; Length 11;
Best Local Similarity 71.4%; Pred. No. 9.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 97 GDFTRGD 103
Db 5 GDYVRGD 11

RESULT 38
US-10-601-837-103
Sequence 103, Application US/10601837
Publication No. US20040053309A1
GENERAL INFORMATION:
APPLICANT: Holt, Gordon D
APPLICANT: Kelly, Michael D
APPLICANT: Kennedy, Sandra J
APPLICANT: Moyses, Christopher
TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidn
FILE REFERENCE: 2543-1-030
CURRENT APPLICATION NUMBER: US/10/601,837
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: PCI/GB01/05777
PRIOR FILING DATE: 2001-12-24
PRIOR APPLICATION NUMBER: US 60/260392
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 12
TYPE: PRT
ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-103

Query Match 3.0%; Score 32; DB 12; Length 12;
Best Local Similarity 60.0%; Pred. No. 1e+04;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 96 GGDFTRGDGT 105
Db 2 GGPFCAQDAT 11

```

; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIC
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-991-225-38

Query Match      3.0%; Score 32; DB 10; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      146 ITTVKTAWL 154
DB      4 VTSIRSAWI 12

RESULT 42
US-10-369-405-19
; Sequence 19, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRENMY11, AND VARIANTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0075A CIP
; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-10-369-405-19

Query Match      3.0%; Score 32; DB 12; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      146 ITTVKTAWL 154
DB      4 VTSIRSAWI 12

RESULT 43
US-10-369-405-38
; Sequence 38, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRENMY11, AND VARIANTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0075A CIP
; ORGANISM: Homo sapiens
US-10-369-405-38

; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-991-225-38

Query Match      3.0%; Score 32; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      185 PLKDVIIADCGK 196
DB      1 PTPVWIRCGK 12

RESULT 40
US-09-991-225-19
; Sequence 19, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIC
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-09-991-225-19

Query Match      3.0%; Score 32; DB 10; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      146 ITTVKTAWL 154
DB      4 VTSIRSAWI 12

RESULT 41
US-09-991-225-38
; Sequence 38, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075A CIP
; ORGANISM: Homo sapiens
US-09-991-225-38
```

```
; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-405-38
```

```
Query Match          3.0%; Score 32; DB 12; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      146 ITTVKTAWL 154
Db       4 VISIRSAWI 12
```

```
RESULT 44
US-10-224-999A-2931
; Sequence 2931, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2931
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2931
```

```
Query Match          3.0%; Score 32; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      185 PLKDVIIADCGK 196
Db       2 PTAPVIRRCGK 13
```

```
RESULT 45
US-10-224-999A-2932
; Sequence 2932, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
```

```
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2932
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2932
```

```
Query Match          3.0%; Score 32; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      185 PLKDVIIADCGK 196
Db       1 PTAPVIRRCGK 12
```

```
Search completed: August 30, 2004, 11:05:02
Job time : 255.378 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 82.2162 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-44
Perfect score: 1083
Sequence: 1 MKVLLAALAGSVFFLLP.....VIIADCGKIEVEKFAIKE 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	3.5	9	2	US-08-658-639-10
2	38	3.5	9	3	US-08-944-604-10
3	37	3.4	12	2	US-08-556-597-40
4	37	3.4	14	5	PCT-US93-06751-120
5	36	3.3	13	3	US-09-261-855-9
6	35	3.2	9	1	US-07-963-324-2
7	35	3.2	14	2	US-08-448-418-101
8	35	3.2	14	4	US-09-146-979-101
9	33.5	3.1	12	2	US-08-973-563A-25
10	33.5	3.1	12	2	US-08-973-559-25
11	33.5	3.1	12	3	US-08-993-235-5
12	33.5	3.1	12	4	US-08-993-235-5
13	33	3.0	8	1	US-08-482-880-23
14	33	3.0	8	2	US-08-273-274-23
15	33	3.0	8	2	US-08-475-041-23
16	33	3.0	8	2	US-08-484-773-23
17	33	3.0	8	2	US-08-361-864-27
18	33	3.0	9	2	US-08-335-812-23
19	33	3.0	9	2	US-08-753-781-36
20	33	3.0	9	3	US-09-141-127-19
21	33	3.0	10	2	US-08-658-639-8
22	33	3.0	10	3	US-08-944-604-8
23	33	3.0	10	4	US-09-269-991B-10
24	33	3.0	14	2	US-08-656-906-26
25	33	3.0	14	3	US-09-217-847-26
26	32.5	3.0	12	2	US-08-973-563A-27
27	32.5	3.0	12	2	US-08-973-559-27

28	32.5	3.0	12	3	US-08-993-235-7	Sequence 7, Appli
29	32.5	3.0	12	4	US-08-993-235-7	Sequence 7, Appli
30	32.5	3.0	13	3	US-08-394-748A-4	Sequence 4, Appli
31	32.5	3.0	13	3	US-08-916-913A-7	Sequence 7, Appli
32	32.5	3.0	13	4	US-09-591-564-7	Sequence 4, Appli
33	32.5	3.0	13	5	PCT-US95-02478-4	Sequence 4, Appli
34	32	3.0	8	1	US-08-271-830-56	Sequence 56, Appli
35	32	3.0	8	2	US-08-416-870C-15	Sequence 15, Appli
36	32	3.0	9	2	US-08-232-539D-32	Sequence 32, Appli
37	32	3.0	9	3	US-08-466-151-50	Sequence 50, Appli
38	32	3.0	9	4	US-08-466-163B-50	Sequence 50, Appli
39	32	3.0	9	4	US-09-802-096-50	Sequence 9, Appli
40	32	3.0	10	2	US-08-464-025A-9	Sequence 9, Appli
41	32	3.0	10	3	US-08-466-151-17	Sequence 17, Appli
42	32	3.0	10	3	US-08-466-151-46	Sequence 46, Appli
43	32	3.0	10	4	US-08-466-163B-17	Sequence 17, Appli
44	32	3.0	10	4	US-08-466-163B-46	Sequence 46, Appli
45	32	3.0	10	4	US-09-755-630B-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1
US-08-658-639-10
; Sequence 10, Application US/08658639
; Patent No. 5914238
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,639
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-639-10

Query Match 3.5%; Score 38; DB 2; Length 9;
Best Local Similarity 87.5%; Pred No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0;
Qy 189 VIIADCGK 196
| | | | |
Db 1 VIIADCGE 8

```

RESULT 2
US-08-944-604-10
; Sequence 10, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESER, SUSAN
; APPLICANT: OSAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,604
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-604-10

Query Match 3.5%; Score 38; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 0;

QY 189 VIIADCGK 196
Db 1 VIIADCGE 8

RESULT 3
US-08-556-597-40
; Sequence 40, Application US/08556597
; Patent No. 587155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-40

Query Match 3.4%; Score 37; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.7e+02; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 4;

QY 156 GKVVVFGKVLG 167
Db 1 GLAVTFGSVLG 12

RESULT 4
PCT-US93-06751-120
; Sequence 120, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMP and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Beta
PCT-US93-06751-120
Query Match 3.4%; Score 37; DB 5; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 120 FKLKHGPG 128
Db 3 YRAHYGPG 11

RESULT 5
US-09-261-855-9
; Sequence 9, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for SEQ ID NOS:3-8.
US-09-261-855-9

Query Match 3.3%; Score 36; DB 3; Length 13;
Best Local Similarity 63.6%; Pred. No. 1.3e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 97 GDFTRGDTGG 107
Db 3 GGFGRGGG 13

RESULT 6
US-09-963-324-2
; Sequence 2, Application US/07963324
; Patent No. 5274122
; GENERAL INFORMATION:
; APPLICANT: Marburg, Stephen
; APPLICANT: Leanza, William J
; APPLICANT: Tolman, Richard L
; TITLE OF INVENTION: Acidic Derivatives of Homocysteine
; TITLE OF INVENTION: Thiolactone
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,324
; FILING DATE: 19921015
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: 18787
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3901
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Nle
; OTHER INFORMATION: /note= "norleucine"
; FEATURE:
; NAME/KEY: Cross-links
; LOCATION: 2..9
; OTHER INFORMATION: /label= cycle
; OTHER INFORMATION: /note= "amide bond through Lys epsilon amino"
US-07-963-324-2

Query Match 3.2%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 122 LKHVGP 128
Db 1 LKHVGP 7

RESULT 7
US-08-448-418-101
; Sequence 101, Application US/08448418
; Patent No. 5837242
; GENERAL INFORMATION:
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Hoogenboom, Hendricus RJM
; APPLICANT: Malmqvist, Magnus
; APPLICANT: Marks, James D
; APPLICANT: McGuinness, Brian T
; APPLICANT: Pope, Anthony R
; APPLICANT: Prospero, Terence D
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Multivalent and Multispecific Binding
; TITLE OF INVENTION: Proteins, Their Manufacture and Use
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun
; STREET: 6300 Sears Tower 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,418
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 435
; CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02492
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
```

;; APPLICATION NUMBER: GB 9225453.1
;; FILING DATE: 04-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9300816.7
;; FILING DATE: 16-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93303614.7
;; FILING DATE: 10-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9319969.3
;; FILING DATE: 22-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David W. Clough
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 28111/32651
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide linker
US-08-448-418-101

Query Match 3.2%; Score 35; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. NO. 1.8e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 96 GGDFTRGDTGGKS 109
Db 1 GGGGGGGGGGSS 14

RESULT 8
US-09-146-979-101
; Sequence 101, Application US/09146979
; Patent No. 6492123
; GENERAL INFORMATION:
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Hoogenboom, Hendricus RJM
; APPLICANT: Malmqvist, Magnus
; APPLICANT: Marks, James D
; APPLICANT: McGuinness, Brian T
; APPLICANT: Pope, Anthony R
; APPLICANT: Prospero, Terence D
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Multivalent and Multispecific Binding
; TITLE OF INVENTION: Proteins, Their Manufacture and Use
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun
; STREET: 6300 Sears Tower 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,979
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,418
; FILING DATE: 14-MAY-1996
; APPLICATION NUMBER: PCT/GB93/02492
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225453.1
; FILING DATE: 04-DEC-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9300816.7
;; FILING DATE: 16-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93303614.7
;; FILING DATE: 10-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9319969.3
;; FILING DATE: 22-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David W. Clough
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 28111/32651
;; INFORMATION FOR SEQ ID NO: 101:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide linker
US-09-146-979-101

Query Match 3.2%; Score 35; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. NO. 1.8e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 96 GGDFTRGDTGGKS 109
Db 1 GGGGGGGGGGSS 14

RESULT 9
US-08-973-563A-25
; Sequence 25, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note= "At least one amino acid
; OTHER INFORMATION: must have a D configuration."
US-08-973-563A-25

Query Match 3.1%; Score 33.5; DB 2; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 75 EKGFYKNSKPF 86
Db 2 KRHFYKNSKPF 12

RESULT 10
US-08-973-559-25
; Sequence 25, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-559-25

Query Match 3.1%; Score 33.5; DB 2; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 75 EKGFYKNSKPF 86
Db 2 KRHFYKNSKPF 12
```

```
Db 2 KRHFYKNSKPF 12

RESULT 11
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5

Query Match 3.1%; Score 33.5; DB 3; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 75 EKGFYKNSKPF 86
Db 2 KRHFYKNSKPF 12

RESULT 12
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5

Query Match 3.1%; Score 33.5; DB 4; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 75 EKGFYKNSKPF 86
Db 2 KRHFYKNSKPF 12

RESULT 13
US-08-482-880-23
; Sequence 23, Application US/08482880
; Patent No. 5736122
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 33
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,880
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5736122nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,216-L
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-482-880-23

Query Match 3.0%; Score 33; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTGG 107
|||
Db 2 RGDGGGG 8

RESULT 14
US-08-273-274-23
;; Sequence 23, Application US/08273274
;; Patent No. 5849260
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Lister-James, John
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Thrombus Imaging
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Allegretti & Witcoff, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/273,274
;; FILING DATE:
;; CLASSIFICATION: 436
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/886,752
;; FILING DATE: 21-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5849260nan, Kevin E
;; REGISTRATION NUMBER: 35,303

;; REFERENCE/DOCKET NUMBER: 92,216
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-273-274-23

Query Match 3.0%; Score 33; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTGG 107
|||
Db 2 RGDGGGG 8

RESULT 15
US-08-475-041-23
;; Sequence 23, Application US/08475041
;; Patent No. 5879658
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Lister-James, John
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Thrombus Imaging
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/475,041
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5879658nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,216-M
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-475-041-23

Query Match 3.0%; Score 33; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTGG 107
|||
Db 2 RGDGGGG 8

RESULT 16
US-08-484-773-23
; Sequence 23, Application US/08484773
; Patent No. 5968476
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,773
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5968476nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-O
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-773-23

Query Match 3.0%; Score 33; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 RGDGTGG 107
Db 2 RGDGGGG 8

RESULT 17
US-08-361-864-27
; Sequence 27, Application US/08361864
; Patent No. 5977064
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Multimeric Polyvalent Antithrombotic
; TITLE OF INVENTION: Agents
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,864
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,466A
; FILING DATE: 19921002
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5977064nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,668
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-361-864-27

Query Match 3.0%; Score 33; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 RGDGTGG 107
Db 2 RGDGGGG 8

RESULT 18
US-08-335-832-23
; Sequence 23, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-335-832-23

Query Match 3.0%; Score 33; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTGG 107
Db 2 RGDGGGG 8

RESULT 19
US-08-753-781-36
; Sequence 36, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Eladio
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DITI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-753-781-36

Query Match 3.0%; Score 33; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 101 RGDGTGG 107
Db 2 RGDGGGG 8

RESULT 20
US-09-141-127-19
; Sequence 19, Application US/09141127A
; Patent No. 6083481
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBUS IMAGING AGENTS
; FILE REFERENCE: DITI 113.1USC1
; CURRENT APPLICATION NUMBER: US/09/141,127A
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-141-127-19

Query Match 3.0%; Score 33; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 3e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 101 RGDGTGG 107
Db 2 RGDGGGG 8

RESULT 21
US-08-658-639-8
; Sequence 8, Application US/08658639
; Patent No. 5914238
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,639
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-639-8

Query Match 3.0%; Score 33; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 114 RPPDENFKLK 123
Db 1 KFDDENFILR 10

RESULT 22
US-08-944-604-8
; Sequence 8, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.

```
;
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,604
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, THOMAS C
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-944-604-8

Query Match 3.0%; Score 33; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 114 RPPDENFKLK 123
Db 1 KFDDEFILR 10

RESULT 23
US-09-269-991B-10
; Sequence 10, Application US/09269991B
; Patent No. 6686333
; GENERAL INFORMATION:
; APPLICANT: Kashanchi, Fatah
; Sadate, Mohamad Reza
; Brady, John N.
; TITLE OF INVENTION: Inhibition of HIV Replication Using
; Soluble Tat Peptide Analogs
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/269,991B
; FILING DATE: 07-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17704
; FILING DATE: 02-OCT-1997
; APPLICATION NUMBER: US 60/027,658
; FILING DATE: 04-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330

;
; REFERENCE/DOCKET NUMBER: 015280-276100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-269-991B-10

Query Match 3.0%; Score 33; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 KKGPK 33
Db 1 KKGPK 6

RESULT 24
US-08-656-906-26
; Sequence 26, Application US/08656906
; Patent No. 5972901
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,906
; FILING DATE: 03-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/
; FILING DATE: 03-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO WO 95/25809
; FILING DATE: 23-MAR-1995
; APPLICATION NUMBER: US 08/216,534
; FILING DATE: 23-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
```

US-08-656-906-26

Query Match 3.0%; Score 33; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 96 GGDFTRGDTGGKS 109
||| : ||| :
Db 1 GGGGGGGGGGGGS 14

RESULT 25

US-09-217-847-26
; Sequence 26, Application US/09217847
; Patent No. 6200801
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assen-Gallal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,847
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,906
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-09-217-847-26

Query Match 3.0%; Score 33; DB 3; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 96 GGDFTRGDTGGKS 109
||| : ||| :
Db 1 GGGGGGGGGGGGS 14

RESULT 26

US-08-973-563A-27
; Sequence 27, Application US/08973563A
; Patent No. 5895965
; GENERAL INFORMATION:

APPLICANT: Oppenheim, Frank G.
APPLICANT: Xu, Tao
APPLICANT: Spacciapoli, Peter
APPLICANT: Roberts, F. D.
APPLICANT: Friden, Philip M.
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
Peptides
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note= "At least one amino acid
must have a D configuration."

US-08-973-563A-27

Query Match 3.0%; Score 32.5; DB 2; Length 12;
Best Local Similarity 77.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 78 FGYNKSKFH 86
||| : ||| :
Db 5 FGYNKSKFH 12

RESULT 27

US-08-973-559-27
; Sequence 27, Application US/08973559
; Patent No. 5912230
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU, TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides

```
;
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-27

Query Match 3.0%; Score 32.5; DB 2; Length 12;
Best Local Similarity 77.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 78 FGYNKSKFH 86
Db 5 FGYNK-KFH 12

RESULT 28
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7

Query Match 3.0%; Score 32.5; DB 3; Length 12;
Best Local Similarity 77.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 78 FGYNKSKFH 86
Db 5 FGYNK-KFH 12

RESULT 29
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7

Query Match 3.0%; Score 32.5; DB 4; Length 12;
Best Local Similarity 77.8%; Pred. No. 2.7e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 78 FGYNKSKFH 86
Db 5 FGYNK-KFH 12

RESULT 30
US-08-394-748A-4
; Sequence 4, Application US/08394748A
; Patent No. 6013628
; GENERAL INFORMATION:
; APPLICANT: Skubitz, Amy P.N.
; APPLICANT: Furcht Leo T.
; APPLICANT: Balles, Mark
; APPLICANT: Gregerson, Dale S.
; APPLICANT: Agarwal, Anita
; APPLICANT: Wright, Martha M.
; APPLICANT: Murali, Shobana
; TITLE OF INVENTION: Method for Treating Conditions of the Eye
; TITLE OF INVENTION: Using Polypeptides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6013628west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,748A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/203,458
; FILING DATE: 28-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600.307US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
```

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: Hep-III
US-08-394-748A-4

Query Match 3.0%; Score 32.5; DB 3; Length 13;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 39 YFDLRI-GDE 47
|||||:
Db 4 YFDLRLKGDK 13

RESULT 31
US-08-916-913A-7
Sequence 7, Application US/08916913A
Patent No. 6121027
GENERAL INFORMATION:
APPLICANT: Clapper, David L.
APPLICANT: Swanson, Melvin J.
APPLICANT: Hu, Sheau-Ping
APPLICANT: Amos, Richard A.
APPLICANT: Everson, Terrence P.
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY ACTIVE MOIETIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-97
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,913A
FILING DATE: 15 August 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6121027e
FILING DATE: No. 6121027e
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 9896.116.0
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-913A-7

Query Match 3.0%; Score 32.5; DB 3; Length 13;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 39 YFDLRI-GDE 47
|||||:
Db 4 YFDLRLKGDK 13

RESULT 32
US-09-591-564-7
Sequence 7, Application US/09591564
Patent No. 6514734
GENERAL INFORMATION:
APPLICANT: Clapper, David L.
APPLICANT: Swanson, Melvin J.
APPLICANT: Hu, Sheau-Ping
APPLICANT: Amos, Richard A.
APPLICANT: Everson, Terrence P.
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY ACTIVE MOIETIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fredrikson & Byron, P.A.
STREET: 900 Second Avenue South
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402-3397
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows-97
SOFTWARE: ASCII files
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/591,564
FILING DATE: 09-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,913
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Philip M.
REGISTRATION NUMBER: 31,162
REFERENCE/DOCKET NUMBER: 9896.116.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 347-7088
TELEFAX: (612) 347-7077
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-591-564-7

Query Match 3.0%; Score 32.5; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 39 YFDLRI-GDE 47
|||||:
Db 4 YFDLRLKGDK 13

RESULT 33
PCT-US95-02478-4
Sequence 4, Application PC/TUS9502478
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for Treating Conditions
TITLE OF INVENTION: Of the Eye Using Polypeptides
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: Hep-III
PCT-US95-02478-4

Query Match 3.0%; Score 32.5; DB 5; Length 13;
Best Local Similarity 70.0%; Pred. No. 3e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 39 YFDLRI-GDE 47
|||||: ||:
Db 4 YFDLRLKGDK 13

RESULT 34
US-08-271-830-56
Sequence 56, Application US/08271830
Patent No. 5510332
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Beck, Pamela J.
TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
TITLE OF INVENTION: INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5510332th Stetson, Suite 4700
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271.830
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5510332thrd, Thomas E.
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa=Pro-NH2."
US-08-271-830-56

Query Match 3.0%; Score 32; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 126 GPGWVSM 132
|||||: :
Db 1 GPGWLDV 7

RESULT 35
US-08-416-870C-15
Sequence 15, Application US/08416870C
Patent No. 5824862
GENERAL INFORMATION:
APPLICANT: HIYOSHI, TORU
APPLICANT: MINE, TOSHIKI
APPLICANT: KASAKA, KEISUKE
APPLICANT: TYSON, ROBERT HUM
APPLICANT: PAGE, ANTHONY MILES JOHN
TITLE OF INVENTION: DNA ENCODING ATP-DEPENDENT FRUCTOSE 6-PHOSPHATE
TITLE OF INVENTION: 1-PHOSPHOTRANSFERASE ORIGINATING FROM PLANT, RECOMBINANT VECTOR
TITLE OF INVENTION: SAME AND METHOD FOR CHANGING SUGAR CONTENT IN PLANT CELLS UNDER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALL CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416.870C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760-195P(PCT)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-416-870C-15

Query Match 3.0%; Score 32; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 62 PKTVDN 67
|||||: ||:
Db 1 PKTIDN 6

RESULT 36
US-08-232-539D-32
Sequence 32, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardiou, Paula M.
TITLE OF INVENTION: IGE Antagonists
NUMBER OF SEQUENCES: 60

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/232,539D
;; FILING DATE: 21-Apr-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION NUMBER:
;; APPLICATION NUMBER: 08/178583
;; FILING DATE: 07-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718P3
;; TELEPHONE: 650/225-1489
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-232-539D-32

Query Match 3.0%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||
Db 4 WLDGK 8

RESULT 37
US-08-466-151-50
; Sequence 50, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995

;; APPLICATION NUMBER: 08/405617
;; FILING DATE: 15-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/185899
;; FILING DATE: 26-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/879495
;; FILING DATE: 07-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39,044
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1489
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-466-151-50

Query Match 3.0%; Score 32; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||
Db 4 WLDGK 8

RESULT 38
US-08-466-163B-50
; Sequence 50, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of Ige Fc(epsilon)3 fragment
US-08-466-163B-50

Query Match 3.0%; Score 32; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||
Db 4 WLDGK 8

RESULT 39
US-09-802-096-50

```
; Sequence 50, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE (epsilon)3 fragment
US-09-802-096-50

Query Match          3.0%; Score 32; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157
Db 4 WLDGK 8

RESULT 40
US-08-464-025A-9
; Sequence 9, Application US/08464025A
; Patent No. 5994514
; GENERAL INFORMATION:
; APPLICANT: Jardieu et al.
; TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,025A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
```

```
US-08-464-025A-9

Query Match          3.0%; Score 32; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157
Db 5 WLDGK 9

RESULT 41
US-08-466-151-17
; Sequence 17, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-17

Query Match          3.0%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 153 WLDGK 157
Db 5 WLDGK 9
```

RESULT 42
US-08-466-151-46
; Sequence 46, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-46

Query Match 3.0%; Score 32; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||||
Db 5 WLDGK 9

RESULT 43
US-08-466-163B-17
; Sequence 17, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06

; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-466-163B-17

Query Match 3.0%; Score 32; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||||
Db 5 WLDGK 9

RESULT 44
US-08-466-163B-46
; Sequence 46, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 46
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant sequence substituted in place of IgE Fc(epsilon)3 fragment
US-08-466-163B-46

Query Match 3.0%; Score 32; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WLDGK 157
|||||
Db 5 WLDGK 9

RESULT 45
US-09-755-630B-33
; Sequence 33, Application US/09755630B
; Patent No. 6639054
; GENERAL INFORMATION:
; APPLICANT: ALIBHAI, MURTAZA F.
; APPLICANT: ASTWOOD, JAMES D.
; APPLICANT: SAMPSON, HUGH A.
; APPLICANT: MCWHERTER, CHARLES A.
; TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTAINS
; FILE REFERENCE: 11899.0217.NFUS00 (MCB2117)
; CURRENT APPLICATION NUMBER: US/09/755,630B

```
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,669
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-33
```

```
Query Match      3.0%; Score 32; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      201 KPFAIAKE 208
      :||| |||
Db      3 RPFPAAKE 10
```

```
Search completed: August 30, 2004, 10:57:21
Job time : 83.2162 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38,898 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIXDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	36	92.3	9	3	AAV69962 Human cyc
2	36	92.3	9	3	AAV69960 Human cyc
3	36	92.3	9	3	AAV69921 Human cyc
4	36	92.3	9	4	AB446946 Human cyc
5	36	92.3	9	4	AB446930 Human cyc
6	36	92.3	9	4	AB446908 Human cyc
7	36	92.3	9	5	ABG79075 Human Cyp
8	36	92.3	9	6	ABR84373 Human Cyp
9	36	92.3	9	7	ADCl17701 Cyclophil
10	36	92.3	9	8	AD89641 Class I H
11	28	71.8	9	5	ABG94771 Replikin
12	28	71.8	9	5	ABG94772 Replikin
13	28	71.8	9	6	ABU57321 Replikin
14	28	71.8	9	6	ABU57322 Replikin
15	28	71.8	9	7	AD888394 Tumour vi
16	28	71.8	9	7	AD888395 Tumour vi
17	28	71.8	9	7	AD888396 Tumour vi
18	28	71.8	9	7	AD888397 Tumour vi
19	27	69.2	12	2	AAW92359 CYP2B1 im
20	25	64.1	7	8	ADf66836 Human his
21	25	64.1	10	8	ADf66861 Murine hi
22	25	64.1	10	8	ADf66867 Human his
23	25	64.1	11	3	AAV69924 Human cyc
24	25	64.1	12	8	AD033999 Fucosyltr
25	25	61.5	9	5	ABG32837 PP2AA-bin

26	24	61.5	9	5	ABG32836	Abg32836	PP2AA-bin
27	23	59.0	10	2	AAV69521	Aar96521	Hepatitis
28	23	59.0	10	8	ADf66227	Adp26227	Plasmodiu
29	23	59.0	11	2	AAV48203	Aar48203	Human pho
30	23	59.0	11	2	AAW67692	Aaw67692	LXXLL sig
31	23	59.0	11	4	AAW82292	Aab82292	Phosphory
32	23	59.0	11	6	ABU57332	Abu57332	Replikin
33	23	59.0	11	7	ADD88405	Add88405	Transform
34	23	59.0	11	7	ADG18183	Adg18183	Transform
35	23	59.0	12	1	AAV93365	Aap93365	Amino aci
36	23	59.0	12	2	AAV43067	Aay43067	GRIP1 nuc
37	22	56.4	9	2	AAW82306	Aaw82306	Transport
38	22	56.4	9	3	ABR28435	Aab28435	Bacillus
39	22	56.4	9	8	ADN68529	Adn68529	Human 273
40	22	56.4	10	2	AAV92146	Aar92146	Porphyrin
41	22	56.4	10	5	ABV74381	Abb74381	Karyophil
42	22	56.4	12	2	AAV35255	Aar35255	D32.39 an
43	22	56.4	12	2	AAV56723	Aar56723	Random pe
44	22	56.4	12	2	AAV91471	Aar91471	D32.39 no
45	22	56.4	12	2	AAW25253	Aaw25253	Antibody

ALIGNMENTS

RESULT 1
ID AAY69962 standard; peptide; 9 AA.
XX AAY69962;
XX AC
XX 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #42.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX PN WO9967288-Al.
XX PD 29-DEC-1999.
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1999; 98JP-00178449.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITCH/) ITOH K.
XX Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX diagnosis of tumors.
XX Claim 10; Page 60; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B, that
XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX peptides are used for the treatment and diagnosis of tumours

Query Match 92.3%; Score 36; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KXHRVIXDK 8
| |||||

```

Db      1 KYHRVIKD 8

RESULT 2
AAY69960
ID AAY69960 standard; peptide; 9 AA.
XX
AC AAY69960;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #40.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label= Phe, Tyr, Met, Trp
FT Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met
FT
FT
XX WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 4; Page 49; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;

Query Match 92.3%; Score 36; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYHRVIKD 8
DB 1 KYHRVIKD 8

RESULT 4
AAB46946
ID AAB46946 standard; peptide; 9 AA.
XX
AC AAB46946;
XX
DT 04-MAY-2001 (first entry)
XX
DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.
XX
KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.
XX
OS Homo sapiens.
XX
EP EP1074267-A1.
XX
PD 07-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00306263.
XX
PR 22-JUL-1999; 99JP-00207687.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
XX
PI Takasu H, Gotoh M, Yamaoka T;
XX
DR WPI; 2001-193144/20.
XX
XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 19; 25pp; English.

```

XX This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of an
 CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease
 XX
 SQ Sequence 9 AA;
 Query Match 92.3%; Score 36; DB 4; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KXHRVIKD 8
 | | | | |
 DB 1 KXHRVIKD 8
 RESULT 5
 AAB46930
 ID AAB46930 standard; peptide; 9 AA.
 AC AAB46930;
 XX
 DT 04-MAY-2001 (first entry)
 XX
 DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.
 XX
 KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
 KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 KW viral infectious disease; cyclophilin B; human.
 XX
 OS Homo sapiens.
 XX
 DN EP1074267-A1.
 XX
 PD 07-FEB-2001.
 XX
 PF 24-JUL-2000; 2000EP-00306263.
 XX
 PR 22-JUL-1999; 99JP-00207687.
 XX
 FA (SUMU) SUMITOMO PHARM CO LTD.
 XX
 PI Takasu H, Gotoh M, Yamaoka T;
 DR WPI; 2001-193144/20.
 XX
 PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
 PT the manufacture of an agent for the induction of antigen-specific T
 PT cells.
 XX
 PS Disclosure; Page 15; 25pp; English.
 XX
 CC This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of an
 CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete

CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease
 XX
 SQ Sequence 9 AA;
 Query Match 92.3%; Score 36; DB 4; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KXHRVIKD 8
 | | | | |
 DB 1 KXHRVIKD 8
 RESULT 6
 AAG68088
 ID AAG68088 standard; peptide; 9 AA.
 XX
 AC AAG68088;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Antitumor peptide cyclophilin B 84-92.
 XX
 KW Antitumor; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumor specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.
 XX
 OS Homo sapiens.
 XX
 PN JP2001245675-A.
 XX
 PD 11-SEP-2001.
 XX
 PF 25-DEC-2000; 2000JP-00393047.
 XX
 PR 28-DEC-1999; 99JP-00374322.
 XX
 PA (ITOY/) ITO Y.
 XX
 DR WPI; 2001-610076/70.
 XX
 PT New peptides for recognizing cancer cells with tumor specific cytotoxic T
 PT lymphocytes and for treating cancer.
 XX
 PS Claim 8; Page 2; 14pp; Japanese.
 XX
 CC The present invention describes peptides recognising cancer cells with
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
 CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 CC the above mentioned sequences; and (4) peptides with one or more deleted,
 CC substituted, added or inserted amino acid(s) of the above mentioned
 CC sequences, particularly those having recognising property due to HLA-
 CC A2402 binding CTL, especially having at least 5 amino acids, used for
 CC medicine, particularly anticancer agents, derived from antitumor
 CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 CC genes. The antitumor peptides have cytostatic activities. The peptides
 CC are used for the treatment of cancer. The peptides cause activation of
 CC CTL in cancer patients. The present sequence represents a peptide from
 CC the present invention
 XX
 SQ Sequence 9 AA;
 Query Match 92.3%; Score 36; DB 4; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 KXHRVIKD 8
      | | | | |
Db      1 KFHVRVIKD 8

RESULT 7
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (1), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (1) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (1), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (1),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention
XX
SQ Sequence 9 AA;

Query Match          92.3%; Score 36; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KXHRVIKD 8
      | | | | |
Db      1 KFHVRVIKD 8

RESULT 9
ADC17701
ID ADC17701 standard; peptide; 9 AA.
XX
AC ADC17701;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KXHRVIKD 8
      | | | | |
Db      1 KFHVRVIKD 8

RESULT 8
ABR84373
ID ABR84373 standard; peptide; 9 AA.
XX
AC ABR84373;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:23.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.
XX
CC The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match          92.3%; Score 36; DB 6; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KXHRVIKD 8
      | | | | |
Db      1 KFHVRVIKD 8

RESULT 9
ADC17701
ID ADC17701 standard; peptide; 9 AA.
XX
AC ADC17701;
```

XX 18-DEC-2003 (first entry)
 XX Cyclophilin B protein amino acids 84-92.
 XX
 DE cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 XX allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.
 KW
 XX Synthetic.
 OS
 XX WO2003020306-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002WO-JP008641.
 PF
 XX 29-AUG-2001; 2001JP-00260046.
 PR
 XX (ITOH/) ITOH K.
 XX
 PA Itoh K, Yamada A;
 PI
 XX WPI; 2003-300831/29.
 DR
 XX Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.
 PT
 XX Claim 8; SEQ ID NO 1; 49pp; Japanese.
 PS
 XX The invention relates to allergic reaction suppressors, comprising a
 CC peptide which originates from the same antigenic substance as the
 CC antigenic substance inducing the (peptide-originated) allergic reaction,
 CC and containing an epitope different from the epitope participating in the
 CC induction of the allergic reaction and yet does not induce the allergic
 CC reaction. The desensitizers or allergic reaction suppressors are useful
 CC for treating and preventing type I allergic diseases and in cancer
 CC vaccines for preventing or treating cancer. The allergic reaction
 CC suppressors are also useful for suppressing an allergic reaction or
 CC reducing immunoglobulin E antibody production, and for desensitization to
 CC antigens. This sequence represents a peptide used in the invention and
 CC corresponds to amino acids 84-92 of the cyclophilin B protein.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 92.3%; Score 36; DB 7; Length 9;
 Best Local Similarity 87.5%; Pred. NO. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KXHRVVKD 8
 DB 1 KFHVRVKD 8
 RESULT 10
 ADG89641
 ID ADG89641 standard; peptide; 9 AA.
 XX
 AC ADG89641;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Class I HLA-restricted widely expressed antigen #6.
 XX
 DE metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; widely antigen.
 KW
 XX Unidentified.
 OS
 XX WO2003100027-A2.
 PN
 XX

PD 04-DEC-2003.
 XX 28-MAY-2003; 2003WO-US016736.
 PF
 XX 28-MAY-2002; 2002US-0383530P.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA
 XX Wang R;
 PI
 XX WPI; 2004-035134/03.
 DR
 XX Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.
 PT
 XX Disclosure; SEQ ID NO 84; 137pp; English.
 PS
 XX The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted widely expressed
 CC antigen.
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 92.3%; Score 36; DB 8; Length 9;
 Best Local Similarity 87.5%; Pred. NO. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KXHRVVKD 8
 DB 1 KFHVRVKD 8
 RESULT 11
 ABG94771
 ID ABG94771 standard; peptide; 9 AA.
 XX
 AC ABG94771;
 XX
 DT 02-DEC-2002 (first entry)
 XX
 DE Replikin sequence identified by the 3-point recognition method #44.
 XX
 KW Replikin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
 KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
 KW Surface Antigen S Precursor Protein.
 XX
 OS Polyoma virus.
 XX
 PN US2002120106-A1.
 XX
 PD 29-AUG-2002.
 XX
 PF 26-OCT-2001; 2001US-00984056.
 XX
 PR 04-SEP-1998; 98US-00146755.
 PR 27-MAR-2001; 2001US-00817144.
 PR 27-MAR-2001; 2001US-0278761P.
 PR 09-JUL-2001; 2001US-0303396P.
 XX
 XX (BOGO/) BOGOCH S.
 PA (BOGO/) BOGOCH E S.
 XX
 PI Bogoch S, Bogoch ES;
 XX
 DR WPI; 2002-691212/74.
 XX
 PT Isolated Bacillus anthracis and small pox virus peptides (I), also known
 PT as replikins, useful for formulating vaccines for treating anthrax or
 PT small pox, comprise 7 to 50 amino acids.
 PT

XX Disclosure; Page 3; 16pp; English.

PS The invention relates to isolated Bacillus anthracis and small pox virus

XX peptides, also known as replikins, comprising 7 to 50 amino acids

CC including at least one lysine residue located six to ten residues from a

CC second lysine residue, at least one histidine residue, and at least 6%

CC lysine residues. The peptides were identified using the 3-point-

CC recognition method and based on the replikin sequence isolated from

CC glioblastoma cells malignin peptide which is of non-human origin. Also

CC included are anti-replikin antibodies (or antibody cocktail), a method of

CC stimulating the immune system of a subject to produce antibodies to

CC Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-

CC 107) comprising a replikin sequence, an antisense nucleic acid molecule

CC complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.

CC Surface Antigen S Precursor Protein comprising a replikin sequence. The

CC peptides are useful for stimulating the immune system of a subject to

CC produce antibodies that bind specifically to Anthrax or small pox

CC polypeptides containing a replikin sequence. The peptides are useful for

CC generating antibodies that can be used in the treatment and/or prevention

CC of anthrax or small pox. The peptides are also useful for formulating

CC vaccines for treating anthrax or small pox. The present sequence is a

CC replikin sequence isolated by the 3-point-recognition system and sharing

CC structural similarity with the replikin sequence isolated from

CC glioblastoma cells malignin

XX Sequence 9 AA;

XX Query Match 71.8%; Score 28; DB 5; Length 9;

XX Best Local Similarity 62.5%; Pred. No. 1.7e+06;

XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8

Db | | | : | |

1 KQHRELKD 8

RESULT 12

ABG94772

ID ABG94772 standard; peptide; 9 AA.

XX AC ABG94772;

XX DT 02-DEC-2002 (first entry)

XX DE Replikin sequence identified by the 3-point recognition method #45.

XX KW Replikin; Glioma; malignin; anthrax; small pox; antiviral; antibacterial;

XX KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;

XX KW Surface Antigen S Precursor Protein.

XX OS Polyoma virus.

XX US2002120106-A1.

XX PN 29-AUG-2002.

XX PD 26-OCT-2001; 2001US-00984056.

XX PF 04-SEP-1998; 98US-00146755.

XX PR 27-MAR-2001; 2001US-00817144.

XX PR 27-MAR-2001; 2001US-0278761P.

XX PR 09-JUL-2001; 2001US-0303396P.

XX (BOG/) BOGCH S.

PA (BOG/) BOGCH E S.

XX PI Bogoch S, Bogoch ES;

XX WPI; 2002-691212/74.

XX

XX Isolated Bacillus anthracis and small pox virus peptides (I), also known

PT as replikins, useful for formulating vaccines for treating anthrax or

PT small pox, comprise 7 to 50 amino acids.

XX Disclosure; Page 3; 16pp; English.

XX The invention relates to isolated Bacillus anthracis and small pox virus

CC peptides, also known as replikins, comprising 7 to 50 amino acids

CC including at least one lysine residue located six to ten residues from a

CC second lysine residue, at least one histidine residue, and at least 6%

CC lysine residues. The peptides were identified using the 3-point-

CC recognition method and based on the replikin sequence isolated from

CC glioblastoma cells malignin peptide which is of non-human origin. Also

CC included are anti-replikin antibodies (or antibody cocktail), a method of

CC stimulating the immune system of a subject to produce antibodies to

CC Bacillus anthracis or small pox comprising administering an effective

CC amount of at least one or more Bacillus anthracis or small pox replikin

CC and an antisense nucleic acid molecule complementary to a mRNA encoding a

CC Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-

CC 107) comprising a replikin sequence, an antisense nucleic acid molecule

CC complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.

CC Surface Antigen S Precursor Protein comprising a replikin sequence. The

CC peptides are useful for stimulating the immune system of a subject to

CC produce antibodies that bind specifically to Anthrax or small pox

CC polypeptides containing a replikin sequence. The peptides are useful for

CC generating antibodies that can be used in the treatment and/or prevention

CC of anthrax or small pox. The peptides are also useful for formulating

CC vaccines for treating anthrax or small pox. The present sequence is a

CC replikin sequence isolated by the 3-point-recognition system and sharing

CC structural similarity with the replikin sequence isolated from

CC glioblastoma cells malignin

XX Sequence 9 AA;

XX Query Match 71.8%; Score 28; DB 5; Length 9;

XX Best Local Similarity 62.5%; Pred. No. 1.7e+06;

XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8

Db | | | : | |

1 KQHRELKD 8

RESULT 13

ABU57321

ID ABU57321 standard; peptide; 9 AA.

XX AC ABU57321;

XX DT 08-APR-2003 (first entry)

XX DE Replikin peptide sequence #61.

XX KW Replikin; immunostimulant; vaccine; recognin.

XX OS Polyomavirus sp.

XX PN US2002151677-A1.

XX PD 17-OCT-2002.

XX PF 26-OCT-2001; 2001US-00984057.

XX PR 27-MAR-2001; 2001US-0278761P.

XX PR 09-JUL-2001; 2001US-0303396P.

XX (BOG/) BOGCH S.

PA (BOG/) BOGCH E S.

XX PI Bogoch S, Bogoch ES;

XX WPI; 2003-182530/18.

XX

XX New replikins or recognin peptides, useful for stimulating the immune
PT system, and for targeting, labeling or destroying replikin-containing
PT organisms.

XX PS Claim 78; Page 3; 17pp; English.

XX CC The invention describes an isolated replikin or recognin peptide (I)
CC comprising 7-50 amino acids including at least one lysine residue located
CC 6 to 10 residues from a second lysine residue, at least one histidine
CC residue and at least 6% lysine residues. The peptides are useful for
CC stimulating the immune system, and for targeting, labelling or destroying
CC replikin-containing organisms. The computer-readable mediums are useful
CC for identifying a protein or peptide containing a replikin or recognin
CC sequence. This is the amino acid sequence of a replikin peptide
CC identified in the invention

XX SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| | | : | |
Db 1 KQRELKD 8

RESULT 14
ABU57322 standard; peptide; 9 AA.
ID ABU57322
AC ABU57322;
XX 08-APR-2003 (first entry)
XX Replikin peptide sequence #62.
XX Replikin; immunostimulant; vaccine; recognin.
XX Polyomavirus sp.
XX US2002151677-A1.
XX 17-OCT-2002.
XX 26-OCT-2001; 2001US-00984057.
XX 27-MAR-2001; 2001US-0278761P.
XX 09-JUL-2001; 2001US-0303396P.
XX (BOGO/) BOGOCH S.
XX (BOGO/) BOGOCH E S.
XX Bogoch S, Bogoch ES;
XX WPI; 2003-182530/18.
XX New replikins or recognin peptides, useful for stimulating the immune
PT system, and for targeting, labeling or destroying replikin-containing
PT organisms.

XX PS Claim 79; Page 3; 17pp; English.

XX CC The invention describes an isolated replikin or recognin peptide (I)
CC comprising 7-50 amino acids including at least one lysine residue located
CC 6 to 10 residues from a second lysine residue, at least one histidine
CC residue and at least 6% lysine residues. The peptides are useful for
CC stimulating the immune system, and for targeting, labelling or destroying
CC replikin-containing organisms. The computer-readable mediums are useful
CC for identifying a protein or peptide containing a replikin or recognin
CC sequence. This is the amino acid sequence of a replikin peptide
CC identified in the invention

XX SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| | | : | |
Db 1 KQRELKD 8

RESULT 15
ADD88394 standard; peptide; 9 AA.
ID ADD88394
XX ADD88394;
XX 29-JAN-2004 (first entry)
XX Tumour viral Replikin #14.
XX vaccine; gene therapy; malaria; influenza; Replikin; haemagglutinin.
XX Polyomavirus.
XX US2003180328-A1.
XX 25-SEP-2003.
XX 26-MAR-2002; 2002US-00105232.
XX 27-MAR-2001; 2001US-0278761P.
XX 09-JUL-2001; 2001US-0303396P.
XX 26-OCT-2001; 2001US-00984057.
XX (BOGO/) BOGOCH S.
XX (BOGO/) BOGOCH E S.
XX Bogoch S, Bogoch ES;
XX WPI; 2003-852213/79.
XX New Replikin peptides of Plasmodium falciparum or influenza virus, useful
PT for diagnosing, preventing or treating influenza virus infection or
PT malaria.
XX Disclosure; SEQ ID NO 61; 136pp; English.
XX The invention relates to an isolated Plasmodium falciparum peptide or an
CC influenza virus peptide. The composition and methods are useful in
CC diagnosing, preventing or treating influenza virus infection or malaria.
CC Also disclosed is an influenza virus vaccine comprising at least one
CC isolated Replikin present in the haemagglutinin protein of an emerging
CC strain of influenza virus and a pharmaceutical carrier and/or adjuvant
CC and a malaria vaccine comprising at least one isolated P. falciparum
CC Replikin and a pharmaceutical carrier. The present sequence represents
CC the amino acid sequence of a Replikin sequence.

XX SQ Sequence 9 AA;

Query Match 71.8%; Score 28; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVIKD 8
| | | : | |
Db 1 KQRELKD 8

Search completed: October 21, 2004, 07:20:58
Job time : 86 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-37

Perfect score: 39

Sequence: 1 KXHRVIXD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	69.2	12	2	US-08-471-286-1
2	25	64.1	11	1	US-08-378-761A-68
3	25	64.1	11	1	US-08-485-286-68
4	25	64.1	12	4	US-10-037-311B-16
5	23	59.0	10	3	US-08-836-075A-204
6	22	56.4	11	4	US-09-418-780A-14
7	22	56.4	11	4	US-07-778-233B-29
8	22	56.4	12	1	US-07-963-321-29
9	22	56.4	12	1	US-08-290-641-29
10	22	56.4	12	1	US-08-548-540-29
11	22	56.4	12	5	PCT-US96-09809-29
12	22	56.4	12	1	US-08-397-633A-93
13	21	53.8	10	3	US-09-105-839D-72
14	21	53.8	10	4	US-09-344-040C-114
15	21	53.8	10	4	US-07-778-233B-28
16	21	53.8	12	1	US-07-963-321-28
17	21	53.8	12	1	US-08-290-641-28
18	21	53.8	12	1	US-08-548-540-28
19	21	53.8	12	5	PCT-US96-09809-28
20	21	53.8	12	5	PCT-US96-09809-28
21	21	53.8	12	5	PCT-US96-09809-28
22	21	53.8	12	5	PCT-US96-09809-28
23	21	53.8	12	5	PCT-US96-09809-28
24	21	53.8	12	5	PCT-US96-09809-28
25	21	53.8	12	5	PCT-US96-09809-28
26	21	53.8	12	5	PCT-US96-09809-28
27	20	51.3	7	4	US-09-057-363C-26

28 20 51.3 7 4 US-09-265-107-26 Sequence 26, Appl
29 20 51.3 8 3 US-08-893-534A-46 Sequence 46, Appl
30 20 51.3 8 3 US-08-996-679-46 Sequence 46, Appl
31 20 51.3 8 3 US-09-115-395-76 Sequence 76, Appl
32 20 51.3 8 3 US-09-507-102-46 Sequence 46, Appl
33 20 51.3 8 3 US-09-250-059-48 Sequence 48, Appl
34 20 51.3 8 3 US-09-248-074-48 Sequence 48, Appl
35 20 51.3 8 4 US-09-357-717-30 Sequence 30, Appl
36 20 51.3 8 4 US-09-458-870-48 Sequence 48, Appl
37 20 51.3 8 4 US-09-248-015-60 Sequence 60, Appl
38 20 51.3 8 4 US-09-544-782-48 Sequence 48, Appl
39 20 51.3 8 4 US-09-234-395-314 Sequence 314, Appl
40 20 51.3 8 4 US-09-305-928-314 Sequence 314, Appl
41 20 51.3 8 4 US-10-058-821-30 Sequence 30, Appl
42 20 51.3 10 2 US-08-556-597-122 Sequence 122, Appl
43 20 51.3 10 3 US-08-836-075A-205 Sequence 205, Appl
44 20 51.3 11 6 5210075-43 Patent No. 5210075
45 20 51.3 12 3 US-08-742-243-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-471-286-1
; Sequence 1, Application US/08471286
; Patent No. 5866688
; GENERAL INFORMATION:
; APPLICANT: Kim, Hyesook
; APPLICANT: Charnecki, Jonathan
; APPLICANT: Pott, David A.
; APPLICANT: Kim, Edward Y.
; TITLE OF INVENTION: PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
; TITLE OF INVENTION: AGAINST CYTOCHROME P450
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099-4390
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,286
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-301 (Oxford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-286-1

Query Match 69.2%; Score 27; DB 2; Length 12;

Best Local Similarity 83.3%; Pred. No. 17;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HRVIXD 8

Db 7 HRVIXD 12

```
RESULT 2
US-08-378-761A-68
; Sequence 68, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-761A-68

Query Match 64.1%; Score 25; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVVKD 8
Db 3 KKARVVKD 10

RESULT 3
US-08-485-286-68
; Sequence 68, Application US/08485286
; Patent No. 5646026
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US

Query Match 64.1%; Score 25; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVVKD 8
Db 3 KKARVVKD 10

RESULT 4
US-10-037-311B-16
; Sequence 16, Application US/10037311B
; Patent No. 6747190
; GENERAL INFORMATION:
; APPLICANT: MICHIGAN STATE UNIVERSITY
; TITLE OF INVENTION: XYLOGLUCAN FUCCOSYLTRANSFERASES
; FILE REFERENCE: MS00-001C2
; CURRENT APPLICATION NUMBER: US/10/037,311B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US60/117,555
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Cross-species
; US-10-037-311B-16

Query Match 64.1%; Score 25; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVVKD 8
Db 6 HQVIRD 11

RESULT 5
US-08-836-075A-204
; Sequence 204, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
```

```
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-286-68

Query Match 64.1%; Score 25; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVVKD 8
Db 3 KKARVVKD 10

RESULT 4
US-10-037-311B-16
; Sequence 16, Application US/10037311B
; Patent No. 6747190
; GENERAL INFORMATION:
; APPLICANT: MICHIGAN STATE UNIVERSITY
; TITLE OF INVENTION: XYLOGLUCAN FUCCOSYLTRANSFERASES
; FILE REFERENCE: MS00-001C2
; CURRENT APPLICATION NUMBER: US/10/037,311B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US60/117,555
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Cross-species
; US-10-037-311B-16

Query Match 64.1%; Score 25; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVVKD 8
Db 6 HQVIRD 11

RESULT 5
US-08-836-075A-204
; Sequence 204, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
```

TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-204

Query Match 59.0%; Score 23; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 99;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVIKD 8
DB 3 KXHQVTQD 10

RESULT 6
US-09-418-780A-14
; Sequence 14, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-780A-14

Query Match 56.4%; Score 22; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 HRVIK 7
DB 2 HKIHK 6

RESULT 7
US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-418-780A-22

Query Match 56.4%; Score 22; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIK 7
DB 2 HKIHK 6

RESULT 8
US-07-778-233B-29
; Sequence 29, Application US/07778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,233B
; FILING DATE: 19911016
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 26 4 0.8
US-07-778-233B-29

Query Match 56.4%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV1K 7
DB 6 HRVVR 10

RESULT 9

US-07-963-321-29
; Sequence 29, Application US/07963321
; Patent No. 5338665
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,321
; FILING DATE: 19921015
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,223
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 26 4 0.8
US-07-963-321-29

Query Match 56.4%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV1K 7
DB 6 HRVVR 10

RESULT 10

US-08-290-641-29
; Sequence 29, Application US/08290641
; Patent No. 5498530
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,641
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; APPLICATION NUMBER: US 07/778,223
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: 26 4 0.8
US-08-290-641-29

Query Match 56.4%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV1K 7
DB 6 HRVVR 10

RESULT 11

US-08-548-540-29
; Sequence 29, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Steuart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/548,540
;; FILING DATE: 26-OCT-1995
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/290,641
;; FILING DATE: 15-AUG-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/963,321
;; FILING DATE: 15-OCT-1992
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 16528J-001240US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;;
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: 26 4 0.8
;;
;; PCT-US96-09809-29
;;
Query Match 56.4%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIX 7
Db 6 HRVIR 10

RESULT 12
PCT-US96-09809-29
; Sequence 29, Application PC/TUS9609809
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Mallard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US96/09809
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/548,540
;; FILING DATE: 26-OCT-1995
;; APPLICATION NUMBER: US 08/290,641
;; FILING DATE: 15-AUG-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/963,321
;; FILING DATE: 15-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 16528J-001240US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;;
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: 26 4 0.8
;;
;; PCT-US96-09809-29
;;
Query Match 56.4%; Score 22; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIX 7
Db 6 HRVIR 10

RESULT 13
US-08-397-633A-93
; Sequence 93, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; OF ENZYMIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:

```
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-93

Query Match      53.8%; Score 21; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HRVI 6
Db      6 HRVI 9

RESULT 14
US-09-105-839D-72
; Sequence 72, Application US/09105839D
; Patent No. 6287756
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Sahin, Ugur
; APPLICANT: Gure, Ali
; APPLICANT: Old, Lloyd J
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
; FILE REFERENCE: LUD 5556
; CURRENT APPLICATION NUMBER: US/09/105,839D
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-105-839D-72

Query Match      53.8%; Score 21; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KXHRVI 6
Db      5 RLHRII 10

RESULT 15
US-09-344-040C-114
; Sequence 114, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 114
; LENGTH: 10
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-114

Query Match      53.8%; Score 21; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KXHRVI 6
Db      5 RLHRII 10

Search completed: October 21, 2004, 07:29:28
Job time : 22.5 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-37

Perfect score: 39

Sequence: 1 KXHRVIXD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	18	46.2	10	PC4374	telomeric and tetr
2	16	41.0	10	B39308	glycine reductase
3	15	38.5	11	I52708	ELAV-like neuronal
4	15	38.5	12	PT0228	Ig heavy chain CDR
5	15	38.5	12	PC4377	telomeric and tetr
6	14	35.9	7	PT0246	Ig heavy chain CRD
7	14	35.9	9	S78420	ribosomal protein
8	14	35.9	10	B56899	serum heterodimer,
9	14	35.9	11	PT0733	unidentified 6.0/1
10	14	35.9	12	S09082	proteasome chain 1
11	13	33.3	6	S02617	alcohol dehydrogen
12	13	33.3	6	B56979	collagen alpha 1(I
13	13	33.3	7	PT0520	T-cell receptor be
14	13	33.3	8	S63381	cytochrome-c oxida
15	13	33.3	8	S69165	ferredoxin a2 - Ja
16	13	33.3	9	T31612	hypothetical prote
17	13	33.3	9	A42266	peptidylglycine me
18	13	33.3	9	A60427	macrophage cytoox
19	13	33.3	9	S39437	D-amino-acid oxida
20	13	33.3	10	S13224	virG protein - Agr
21	13	33.3	10	T14212	cytochrome-c oxida
22	13	33.3	10	S23307	neurokinin A - ral
23	13	33.3	10	S23186	neurokinin A - Atl
24	13	33.3	11	S23364	T-cell receptor al
25	13	33.3	12	C30503	Ig gamma-2b chain
26	12	30.8	7	I46968	alpha-myosin heavy
27	12	30.8	9	B45796	dihydrolipoamide S
28	12	30.8	9	A61102	parathyroid hormon
29	12	30.8	9	PS0253	glycine cleavage s

ALIGNMENTS

RESULT 1

PC4374

telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999

C:Accession: PC4374

R:Saig, G.; Weisman-Shomer, P.; Fry, M.

Biochem. Biophys. Res. Commun. 237, 617-623, 1997

A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI

A:Reference number: PC4371; MUID:97445086; PMID:9299414

A:Accession: PC4374

A:Molecule type: protein

A:Residues: 1-10 <SAR>

C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 46.2%; Score 18; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 9e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXHRV 5

DB 6 KEHRL 10

RESULT 2

B39308

glycine reductase (EC 1.4.99.-) sulphydryl protein C, beta chain - Clostridium sticklandii

C:Species: Clostridium sticklandii

C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004

C:Accession: B39308

R:Stadman, T.C.; Davis, J.N.

J. Biol. Chem. 266, 22147-22153, 1991

A:Title: Glycine reductase protein C. Properties and characterization of its role in the

A:Reference number: A39308; MUID:92042141; PMID:1939235

A:Accession: B39308

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <STA>

A:Cross-references: UNIPROT:Q9EV92

C:Function:

A:Description: glycine reductase complex catalyzes the reductive deamination of glycine t

C:Keywords: ATP; oxidoreductase

Query Match 41.0%; Score 16; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIXD 8

DB 4 NKVIAD 9

RESULT 3
I52708
N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: I52708
R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis
A;Reference number: I52708
A;Accession: I52708
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-11 <SEK>
A;Cross-references: UNIPROT:Q15234; GB:S73887; NID:G688242; PID:ADL14142.1; PID:G426184
C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
C;Genetics:
A;Gene: GDB:ELAVL4; HUD; PNEM
A;Cross-references: GDB:141875; OMIM:168360
A;Map position: 1p36-1p36
C;Keywords: alternative splicing

Query Match 38.5%; Score 15; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 RVIK 7
DB 6 RILK 9

RESULT 4
PT0228
Ig heavy chain CDR3 region (clone 1-112) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0228
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0228
A;Molecule type: DNA
A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 38.5%; Score 15; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 RVIK 7
DB 6 RILK 9

RESULT 5
PC4377
telomeric and tetraplex DNA binding protein qTPB2 VIII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: PC4377
R;Sargis, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTPB2: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4377
A;Molecule type: protein
A;Residues: 1-12 <SAB>
A;Cross-references: UNIPROT:Q9QX30; UNIPROT:Q9Z0U8; UNIPROT:Q88311; UNIPROT:Q9QX81
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 38.5%; Score 15; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 RVIKD 8
DB 2 RYVRD 6

RESULT 5
PC4377
telomeric and tetraplex DNA binding protein qTPB2 VIII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: PC4377
R;Sargis, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTPB2: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4377
A;Molecule type: protein
A;Residues: 1-12 <SAB>
A;Cross-references: UNIPROT:Q9QX30; UNIPROT:Q9Z0U8; UNIPROT:Q88311; UNIPROT:Q9QX81
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 38.5%; Score 15; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KXHRV 5
DB 3 KPHTV 7

RESULT 6
PT0246
Ig heavy chain CDR3 region (clone 2-103D) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0246
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0246
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.9%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HRVI 6
DB 1 HEVL 4

RESULT 7
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 35.9%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 HRV 5
DB 5 HRL 7

RESULT 8
B56899
serum heterodimer, 24K chain - sandbar shark (fragment)
C;Species: Carcharhinus plumbeus (sandbar shark)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: B56899
R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by
A;Reference number: A56899; MUID:93092592; PMID:1458832
A;Accession: B56899
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <VAZ>
A;Cross-references: UNIPROT:Q7LZJ7

C;Keywords: glycoprotein; plasma

Query Match 35.9%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVIKD 8
|||:
Db 6 RVVNE 10

RESULT 9

PQ0733
unidentified 6.0/15K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0733
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696
A;Accession: PQ0733
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <KOM>

Query Match 35.9%; Score 14; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVI 6
||:
Db 1 HTII 4

RESULT 10

S09082
proteasome chain 1 - rat (fragment)
N;Alternate names: multicatalytic proteinase chain 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09082
R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.
FEBS Lett. 262, 327-329, 1990
A;Title: N-terminal sequence similarities between components of the multicatalytic prote
A;Reference number: S09082; MUID:90242957; PMID:2335214
A;Accession: S09082
A;Molecule type: protein
A;Residues: 1-12 <LIL>
C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 35.9%; Score 14; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VIKD 8
|||:
Db 7 VYKD 10

RESULT 11

S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S02617
R;Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall
FEBS Lett. 222, 99-103, 1987
A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differenc
A;Reference number: S02617; MUID:88005160; PMID:3653405
A;Accession: S02617
A;Molecule type: protein
A;Residues: 1-6 <FAI>

A;Cross-references: UNIPROT:P19854
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 33.3%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VIK 7
|||:
Db 4 VIK 6

RESULT 12

B56979
collagen alpha 1(II) chain - bovine (fragment)
N;Alternate names: collagen alpha 3(XI) chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C;Accession: B56979
R;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Insi
A;Reference number: A56978; MUID:95370194; PMID:7642541
A;Accession: B56979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <WUA>

A;Note: the residue designated "x" is modified lysine in collagen 1(II) some cross-linked

Query Match 33.3%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HR 4
||:
Db 5 HR 6

RESULT 13

PT0520
T-cell receptor beta chain V-D-J region (100-4F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0520
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0520
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 33.3%; Score 13; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXH 3
||:
Db 5 KXH 7

RESULT 14

S65381
cytochrome-c oxidase (EC 1.9.3.1) chain V1b, hepatic - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65381
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65381

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <SCH>

A;Cross-references: UNIPROT:P80430

C;Keywords: oxidoreductase

Query Match 33.3%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HR 4

Db 7 HR 8

RESULT 15

S69165

ferredoxin a2 - Japanese radish (fragment)

C;Species: Kaiware daikon (Japanese radish)

C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 09-Jul-2004

C;Accession: S69165

R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.

Arch. Biochem. Biophys. 316, 797-802, 1995

A;Title: Four ferredoxins from Japanese radish leaves.

A;Reference number: S69164; MUID:95168867; PMID:7864635

A;Accession: S69165

A;Molecule type: protein

A;Residues: 1-8 <OBA>

A;Cross-references: UNIPROT:Q7M1F1

C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 33.3%; Score 13; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HR 4

Db 2 HR 3

Search completed: October 21, 2004, 07:27:57

Job time : 17.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-37
Perfect score: 39
Sequence: 1 KXHRVIXD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	92.3	9	15	US-10-447-161-84
2	36	92.3	9	16	US-10-788-016-1
3	28	71.8	9	9	US-09-984-056-61
4	28	71.8	9	9	US-09-984-056-62
5	28	71.8	9	9	US-09-984-057-61
6	28	71.8	9	9	US-09-984-057-62
7	28	71.8	9	14	US-10-105-232-61
8	28	71.8	9	14	US-10-105-232-62
9	28	71.8	9	14	US-10-189-437-61
10	28	71.8	9	14	US-10-189-437-62
11	24	61.5	9	14	US-10-211-207-23
12	24	61.5	9	14	US-10-211-207-24
13	24	61.5	9	14	US-10-077-106-23
14	24	61.5	9	14	US-10-077-106-24

15	23	59.0	10	9	US-09-851-138-204	Sequence 204, App
16	23	59.0	11	9	US-09-984-056-72	Sequence 72, Appl
17	23	59.0	11	9	US-09-984-057-72	Sequence 72, Appl
18	23	59.0	11	14	US-10-105-232-72	Sequence 72, Appl
19	23	59.0	11	14	US-10-189-437-72	Sequence 145, App
20	22	56.4	10	10	US-09-876-904A-145	Sequence 14, Appl
21	22	56.4	11	14	US-10-293-822-14	Sequence 22, Appl
22	22	56.4	11	14	US-10-293-822-22	Sequence 4, Appl
23	22	56.4	12	14	US-10-300-575-4	Sequence 76, Appl
24	22	56.4	12	15	US-10-601-953-76	Sequence 14, Appl
25	21	53.8	9	14	US-10-119-536A-14	Sequence 500, App
26	21	53.8	10	10	US-09-876-904A-500	Sequence 114, App
27	21	53.8	10	10	US-09-833-039-114	Sequence 12, Appl
28	21	53.8	10	14	US-10-124-903-12	Sequence 114, App
29	21	53.8	10	14	US-10-177-277-114	Sequence 173, App
30	21	53.8	12	10	US-09-876-904A-173	Sequence 578, App
31	20.5	52.6	11	10	US-09-876-904A-578	Sequence 26, Appl
32	20	51.3	7	14	US-10-369-226-26	Sequence 65, Appl
33	20	51.3	7	17	US-10-459-030B-65	Sequence 54, Appl
34	20	51.3	8	9	US-09-984-056-54	Sequence 314, App
35	20	51.3	8	9	US-09-234-395-314	Sequence 314, App
36	20	51.3	8	9	US-09-305-928-314	Sequence 54, Appl
37	20	51.3	8	9	US-09-984-057-54	Sequence 48, Appl
38	20	51.3	8	9	US-09-769-145-48	Sequence 46, Appl
39	20	51.3	8	13	US-10-006-982-46	Sequence 48, Appl
40	20	51.3	8	14	US-10-105-008-48	Sequence 30, Appl
41	20	51.3	8	14	US-10-058-821-30	Sequence 54, Appl
42	20	51.3	8	14	US-10-105-232-54	Sequence 60, Appl
43	20	51.3	8	14	US-10-189-437-54	Sequence 48, Appl
44	20	51.3	8	14	US-10-359-546-60	
45	20	51.3	8	15	US-10-425-557-48	

ALIGNMENTS

RESULT 1
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US2004002314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 92.3%; Score 36; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXHRVIXD 8
DB 1 KXHRVIXD 8

RESULT 2
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto

; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophilin B
US-10-788-016-1

Query Match 92.1%; Score 36; DB 16; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXHRVVKD 8
Db 1 KQHRELKD 8

RESULT 3
US-09-984-056-61
; Sequence 61, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-61

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVVKD 8
Db 1 KQHRELKD 8

RESULT 4
US-09-984-056-62
; Sequence 62, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-057-61

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVVKD 8
Db 1 KQHRELKD 8

RESULT 6
US-09-984-057-62
; Sequence 62, Application US/09984057

; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-62

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVVKD 8
Db 1 KQHRELKD 8

RESULT 5
US-09-984-057-61
; Sequence 61, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-057-61

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXHRVVKD 8
Db 1 KQHRELKD 8

RESULT 6
US-09-984-057-62
; Sequence 62, Application US/09984057

Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLIKIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-057-62

Query Match 71.8%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8
||| :||
Db 1 KQRELKD 8

RESULT 7
US-10-105-232-61
; Sequence 61, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-61

Query Match 71.8%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8
||| :||
Db 1 KQRELKD 8

RESULT 8
US-10-105-232-62
; Sequence 62, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-62

Query Match 71.8%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8
||| :||
Db 1 KQRELKD 8

RESULT 9
US-10-189-437-61
; Sequence 61, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-61

Query Match 71.8%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVTKD 8

```
Db      1 KQHRELKD 8
|||:|
RESULT 10
US-10-189-437-62
; Sequence 62, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-62
Query Match      71.8%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 KXHRVVKD 8
|||:|
Db      1 KQHRELKD 8
|||:|
RESULT 11
US-10-211-207-23
; Sequence 23, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyomavirus small
US-10-211-207-23
Query Match      61.5%; Score 24; DB 14; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HRVVKD 8
|||:|
Db      1 HRELKD 6
|||:|
RESULT 12
US-10-211-207-24
; Sequence 24, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyomavirus medium
US-10-211-207-24
Query Match      61.5%; Score 24; DB 14; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HRVVKD 8
|||:|
Db      1 HRELKD 6
|||:|
RESULT 13
US-10-077-106-23
; Sequence 23, Application US/10077106
; Publication No. US20030166531A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/077,106
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,757
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyomavirus small
US-10-077-106-23
Query Match      61.5%; Score 24; DB 14; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HRVVKD 8
|||:|
Db      1 HRELKD 6
|||:|
RESULT 14
US-10-077-106-24
; Sequence 24, Application US/10077106
; Publication No. US20030166531A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; TITLE OF INVENTION: PP2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/077,106
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,757
; FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyomavirus medium
US-10-077-106-24

Query Match      61.5%; Score 24; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HRVIXD 8
      ||:|
Db      1 HRELXD 6

RESULT 15
US-09-851-138-204
; Sequence 204, Application US/09851138
; Publication No. US20020183508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
;          STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
;          AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
;          AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P. O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204

Query Match      59.0%; Score 23; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 KXHRVIXD 8
      ||:|
Db      3 KYHQVTQD 10

Search completed: October 21, 2004, 07:33:41
Job time : 52.75 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-37

Perfect score: 39

Sequence: 1 KXHRVIXDX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	53.8	8	Q8AWV7	Q8awv7 anas platyr
2	21	53.8	8	Q8AWV8	Q8awv8 cygnus colu
3	21	53.8	8	Q8AWV9	Q8awv9 anser caeru
4	21	53.8	8	Q8AWW0	Q8aww0 coscoroba c
5	20	51.3	8	Q05403	Q05403 saccharomyc
6	19	48.7	9	Q7SCD2	Q7scd2 neurospora
7	19	48.7	10	Q8N6B1	Q8n6b1 homo sapien
8	19	48.7	10	Q8R1F1	Q8r1f1 pseudomonas
9	19	48.7	11	Q9XSP2	Q9xsp2 hyllobates s
10	19	48.7	11	Q9XSP5	Q9xsp5 pan troglod
11	19	48.7	11	Q9XSP6	Q9xsp6 pongo pygna
12	19	48.7	11	Q9XSP7	Q9xsp7 pygathrix n
13	19	48.7	11	Q9XSP8	Q9xsp8 presbytis j
14	19	48.7	11	Q9XSQ4	Q9xsq4 gorilla gor
15	18	46.2	12	Q7RGL4	Q7rgl4 plasmodium
16	17	43.6	9	Q9TQX7	Q9tqx7 manduca sex
17	17	43.6	10	Q9TQV4	Q9tqv4 e equus cab
18	17	43.6	11	Q8MEL7	Q8mel7 sida hooker
19	17	43.6	11	Q8MEL9	Q8mel9 pavonia has
20	17	43.6	11	Q8MEM2	Q8mem2 lagunaria p
21	17	43.6	11	Q8MEP0	Q8mep0 hibiscus pe
22	17	43.6	11	Q8MEP3	Q8mep3 hibiscus no
23	17	43.6	11	Q8MEP5	Q8mep5 hibiscus mi
24	17	43.6	11	Q8MEQ7	Q8meq7 hibiscus dr
25	17	43.6	11	Q8MER0	Q8mer0 hibiscus co
26	17	43.6	11	Q8MER1	Q8mer1 hibiscus ca
27	17	43.6	11	Q8MER7	Q8mer7 fioria vici
28	17	43.6	11	Q8MER8	Q8mer8 dombeya til
29	17	43.6	11	Q8MES1	Q8mes1 alyogyne pi
30	17	43.6	11	Q8MES3	Q8mes3 alyogyne cr
31	17	43.6	11	Q8MES5	Q8mes5 abelmoschus

32	17	43.6	12	Q8HU93	Q8hu93 bryum donia
33	17	43.6	12	Q8LU67	Q8lu67 macrostelia
34	17	43.6	12	Q8MEL6	Q8mel6 thespesia t
35	17	43.6	12	Q8MEL8	Q8mel8 radyera far
36	17	43.6	12	Q8MEM0	Q8mem0 malvaviscus
37	17	43.6	12	Q8MEM1	Q8mem1 malva negle
38	17	43.6	12	Q8MEM4	Q8mem4 hibiscus zo
39	17	43.6	12	Q8MEM5	Q8mem5 hibiscus wa
40	17	43.6	12	Q8MEM6	Q8mem6 hibiscus tr
41	17	43.6	12	Q8MEM7	Q8mem7 hibiscus ti
42	17	43.6	12	Q8MEM8	Q8mem8 hibiscus sy
43	17	43.6	12	Q8MEM9	Q8mem9 hibiscus su
44	17	43.6	12	Q8MEN0	Q8men0 hibiscus st
45	17	43.6	12	Q8MEN1	Q8men1 hibiscus st

ALIGNMENTS

RESULT 1
Q8AWV7 ID Q8AWV7 PRELIMINARY; PRT; 8 AA.
AC Q8AWV7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Anas platyrhynchos (domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123327; AAM96901.1; --
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 53.8%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIXD 8
|::|
Db 2 HKIVAD 7

RESULT 2
Q8AWV8 ID Q8AWV8 PRELIMINARY; PRT; 8 AA.
AC Q8AWV8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Cygnus columbianus (tundra swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
OX NCBI_TaxID=110926;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123326; AAM96900.1; --
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;
Query Match 53.8%; Score 21; DB 2; Length 8;

```
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIKD 8
Db |:::|
2 HKIVAD 7

RESULT 3
Q8AWV9 PRELIMINARY; PRT; 8 AA.
AC Q8AWV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Anser caerulescens caerulescens (snow goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=70340;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotten J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123325; AAM96899.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match 53.8%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIKD 8
Db |:::|
2 HKIVAD 7

RESULT 4
Q8AWW0 PRELIMINARY; PRT; 8 AA.
AC Q8AWW0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE LDH-B (Fragment).
GN Name=LDH-B;
OS Coscoroba coscoroba (Coscoroba swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
OX NCBI_TaxID=8863;
RN [1]
RP SEQUENCE FROM N.A.
RA Cotten J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123324; AAM96898.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match 53.8%; Score 21; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIKD 8
Db |:::|
2 HKIVAD 7

RESULT 5
Q05403 PRELIMINARY; PRT; 8 AA.
ID Q05403
```

```
Q05403;
AC Q05403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Orf 00915 protein (Fragment).
GN Name=orf 00915;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zamstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B532D2C441E058 CRC64;

Query Match 51.3%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIK 7
Db |:::|
3 HNVVK 7

RESULT 6
Q7SCD2 PRELIMINARY; PRT; 9 AA.
AC Q7SCD2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Predicted protein.
GN Name=NCU05334.;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=514.;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex D.A., Mannhaupt G., Ebboie D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 010-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AABX01000130; EAA34319.1; -.
SQ SEQUENCE 9 AA; 1173 MW; C483A32B50440449 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 3 HRVIK 8
: :
3 NRIYK 8

Db

RESULT 7

Q8NGB1 PRELIMINARY; PRT; 10 AA.

AC Q8NGB1; 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Capacitative calcium channel protein Trp1 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Late pregnancy myometrium;

RA MEDLINE=22181008; PubMed=12193412;

RA Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,

RA Sandorn B.N.;

RT "Multiple Trp isoforms implicated in capacitative calcium entry are

RT expressed in human pregnant myometrium and myometrial cells.";

RL Biol. Reprod. 67:988-994(2002).

DR EMBL; AF483646; AAM97861.1; -.

FT NON_TER 1

SQ SEQUENCE 10 AA; 1336 MW; 0DD0C0B401F40724 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 2.9e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIK 7
: :
6 HRDIX 10

Db

RESULT 8

Q8RJF1 PRELIMINARY; PRT; 10 AA.

AC Q8RJF1; 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Porin-like protein (Fragment).

OS Pseudomonas fluorescens.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=294;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NC16-2, TC29-5, and TC97;

RA MEDLINE=22315381; PubMed=12427948;

RA Kholodii G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;

RT "Tn5041-like transposons: molecular diversity, evolutionary

RT relationships and distribution of distinct variants in environmental

RT bacteria.";

RL Microbiology 148:3569-3582(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=NC16-2, TC29-5, and TC97;

RA Kholodii G.Y.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ422128; CAD19527.1; -.

DR EMBL; AJ422129; CAD19528.1; -.

DR EMBL; AJ422130; CAD19529.1; -.

DR GO:0016021; C:integral to membrane; IEA.

DR GO:0005741; C:mitochondrial outer membrane; IEA.

DR GO:0015288; F:porin activity; IEA.

FW Porin.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1206 MW; 23C47E7401F5A417 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 2.9e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXHRVik 7
: :
4 RSHRPIR 10

Db

RESULT 9

Q9XSP2 PRELIMINARY; PRT; 11 AA.

AC Q9XSP2; 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE Platelet-derived growth factor A chain (Fragment).

GN Name=PDGFA;

OS Hylbaes syndactylus (Siamang) (Symphalangus syndactylus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.

OX NCBI_TaxID=9590;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20065871; PubMed=10598812;

RA Bonthron D.T., Smith S.L., Campbell R.;

RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";

RL Hum. Genet. 105:452-459(1999).

DR EMBL; AJ243280; CAB45927.1; -.

FT NON_TER 1

FT NON_TER 11

SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIK 7
: :
7 HRSVK 11

Db

RESULT 10

Q9XSP5 PRELIMINARY; PRT; 11 AA.

AC Q9XSP5; 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE Platelet-derived growth factor A chain (Fragment).

GN Name=PDGFA;

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20065871; PubMed=10598812;

RA Bonthron D.T., Smith S.L., Campbell R.;

RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";

RL Hum. Genet. 105:452-459(1999).

DR EMBL; AJ243277; CAB45926.1; -.

FT NON_TER 1

FT NON_TER 11

SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 3.2e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIK 7
: :
7 HRSVK 11

Db

```

Db          || :|
            7 HRSVK 11

RESULT 11
Q9XSP6      PRELIMINARY;      PRT;      11 AA.
AC Q9XSP6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243279; CAB45925.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVik 7
Db || :|
7 HRSVK 11

RESULT 12
Q9XSP7      PRELIMINARY;      PRT;      11 AA.
AC Q9XSP7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243282; CAB45924.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVik 7
Db || :|
7 HRSVK 11

RESULT 13
Q9XSP8      PRELIMINARY;      PRT;      11 AA.
AC Q9XSP8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Presbytis johni.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Presbytis.
OX NCBI_TaxID=98375;
RN [1]
RP MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243281; CAB46013.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVik 7
Db || :|
7 HRSVK 11

RESULT 14
Q9XSQ4      PRELIMINARY;      PRT;      11 AA.
AC Q9XSQ4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243278; CAB45916.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 48.7%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVik 7
Db || :|
7 HRSVK 11

RESULT 15
Q7RGL4      PRELIMINARY;      PRT;      12 AA.
AC Q7RGL4;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).

```

```
GN Name=PY04332;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalton S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RL parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL: ABLO1001307; EAA16180.1; -.
DR Hypothetical protein.
KW NON_TER 12 12
FT SEQUENCE 12 AA; 1485 MW; D2A760BC2E633DC2 CRC64;
SQ
Query Match 46.2%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 3 HRV1K 7
DB 3 HKVAK 7
|:|
|:|
Search completed: October 21, 2004, 07:26:47
Job time : 87 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-38

Perfect score: 40

Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	9	3	AAY69963 Human cyc
2	37	92.5	9	3	AAY69958 Human cyc
3	37	92.5	9	3	AAY69961 Human cyc
4	37	92.5	9	3	AAY69922 Human cyc
5	37	92.5	9	4	AAB46947 Human cyc
6	37	92.5	9	4	AAB46931 Human cyc
7	37	92.5	9	4	AAG68089 Antitumou
8	37	92.5	9	5	ABG79076 Human Cyc
9	37	92.5	9	6	ABR84374 Human Cyc
10	37	92.5	9	7	ADCL17709 Modified
11	37	92.5	9	7	ADCL17702 Cyclophil
12	37	92.5	9	8	ADG89642 Class I H
13	27	67.5	9	3	AAY69957 Human cyc
14	25	62.5	8	3	AAB12089 Ad7 cel p
15	25	62.5	8	7	ADB84662 Adenoviru
16	25	62.5	9	2	AAR20729 Pancreat
17	25	62.5	9	3	AAY51905 Elastase
18	25	62.5	10	5	AAY78392 Biosurfac
19	24	60.0	9	8	ADK07318 Hepatitis
20	24	60.0	9	8	ADK06815 Hepatitis
21	23	57.5	6	2	AAR83889 Peptide s
22	23	57.5	11	2	AAB48850 Human pro
23	22	55.0	9	4	AAB45861 Human tum
24	22	55.0	10	6	ABR83253 H. pylori
25	22	55.0	11	8	ADN17045 Gi-alpha

26	22	55.0	12	6	ABR01459 Human TIM
27	22	55.0	12	7	ABR63060 Pathogen
28	21	52.5	5	6	AAR34120 Gluten sp
29	21	52.5	8	2	AAR93207 New contr
30	21	52.5	9	2	AAR72938 E. coli P
31	21	52.5	9	2	AAR72894 E. coli P
32	21	52.5	9	6	ABR67369 Human hsp
33	21	52.5	9	6	ABR67364 Human hsp
34	21	52.5	9	8	ADK07060 Hepatitis
35	21	52.5	10	2	AAR72949 E. coli P
36	21	52.5	10	2	AAR72905 E. coli P
37	21	52.5	10	2	AAR72905 E. coli P
38	21	52.5	10	3	AAB35991 Sorbitol
39	21	52.5	10	3	AAB35991 Sorbitol
40	21	52.5	10	4	AAG87272 Saccharom
41	21	52.5	10	7	ADJ52136 CHI delet
42	21	52.5	10	8	ADK09152 Human pap
43	21	52.5	10	8	ADK09635 Human pap
44	21	52.5	10	8	ADO17328 Different
45	21	52.5	11	2	AAR14821 Bay thioe

ALIGNMENTS

RESULT 1

ID AAY69963 standard; peptide; 9 AA.

XX AC AAY69963;

XX AC (first entry)

DT 11-APR-2000

XX Human cyclophilin B peptide fragment #43.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX OS

PN WO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOH/) ITOH K.

PI Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

XX diagnosis of tumors.

XX Claim 10; Page 60; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The

XX peptides are tumour antigen peptides derived from cyclophilin B, that

XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

XX peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

XX Query Match 92.5%; Score 37; DB 3; Length 9;

XX Best Local Similarity 87.5%; Pred. No. 1.7e+06;

XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 DXMIQGGD 8

XX |||||

```

Db      1 DYMIOGGD 8

RESULT 2
AAV69958
ID AAV69958 standard; peptide; 9 AA.
XX
XX AAY69958;
AC
XX 11-APR-2000 (first entry)
DT
XX Human cyclophilin B peptide fragment #38.
DE
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
OS
XX WO9967288-A1.
PN
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR
XX (SUMU ) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
XX Itoh K, Gomi S;
PI
XX WPI; 2000-116932/10.
DR
XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
XX Claim 4; Page 61; 64pp; Japanese.
PS
XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
XX Sequence 9 AA;
SQ

Query Match 92.5%; Score 37; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYMIOGGD 8
Db 1 DYMIOGGD 8

RESULT 3
AAV69961
ID AAV69961 standard; peptide; 9 AA.
XX
XX AAY69961;
AC
XX 11-APR-2000 (first entry)
DT
XX Human cyclophilin B peptide fragment #41.
DE
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH
XX Misc-difference 2 /label= Phe, Tyr, Met, Trp
FT
XX Misc-difference 9

```

```

FT XX WO9967288-A1.
PN XX 29-DEC-1999.
XX XX 24-JUN-1999; 99WO-JP003360.
XX XX 25-JUN-1998; 98JP-00178449.
XX XX (SUMU ) SUMITOMO PHARM CO LTD.
XX XX (ITOH/) ITOH K.
XX XX Itoh K, Gomi S;
XX XX WPI; 2000-116932/10.
XX XX Tumor antigen peptides derived from cyclophilin E for treatment and
XX XX diagnosis of tumors.
XX XX Claim 10; Page 60; 64pp; Japanese.
XX XX This sequence represents a cyclophilin B peptide of the invention. The
XX XX peptides are tumour antigen peptides derived from cyclophilin B, that
XX XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX XX peptides are used for the treatment and diagnosis of tumours
XX XX
XX XX Sequence 9 AA;
SQ

Query Match 92.5%; Score 37; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
Db 1 DXMIQGGD 8

RESULT 4
AAV69922
ID AAV69922 standard; peptide; 9 AA.
XX
XX AAY69922;
AC
XX 11-APR-2000 (first entry)
DT
XX Human cyclophilin B peptide fragment #2.
DE
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX XX HLA antigen; diagnosis; tumour; therapy.
XX XX Homo sapiens.
XX XX WO9967288-A1.
XX XX 29-DEC-1999.
XX XX 24-JUN-1999; 99WO-JP003360.
XX XX 25-JUN-1998; 98JP-00178449.
XX XX (SUMU ) SUMITOMO PHARM CO LTD.
XX XX (ITOH/) ITOH K.
XX XX Itoh K, Gomi S;
XX XX WPI; 2000-116932/10.
XX XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX XX diagnosis of tumors.
XX XX Claim 4; Page 49; 64pp; Japanese.
XX XX

```

CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match 92.5%; Score 37; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
| | | | |
Db 1 DFMIQGGD 8

RESULT 5
AAB46947
ID AAB46947 standard; peptide; 9 AA.

AC AAB46947;

DT 04-MAY-2001 (first entry)

XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.

XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.

XX Homo sapiens.

XX BP1074267-A1.

XX 07-FEB-2001.

XX 24-JUL-2000; 2000EP-00306263.

XX 22-JUL-1999; 99JP-00207687.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Takasu H, Gotoh M, Yamaoka T;

XX WPI; 2001-193144/20.

XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.

XX Disclosure; Page 20; 25pp; English.

XX This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease

XX Sequence 9 AA;

Query Match 92.5%; Score 37; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
| | | | |
Db 1 DFMIQGGD 8

RESULT 6

AAB46931

ID AAB46931 standard; peptide; 9 AA.

AC AAB46931;

DT 04-MAY-2001 (first entry)

XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.

XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KW viral infectious disease; cyclophilin B; human.

XX Homo sapiens.

XX BP1074267-A1.

XX 07-FEB-2001.

XX 24-JUL-2000; 2000EP-00306263.

XX 22-JUL-1999; 99JP-00207687.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Takasu H, Gotoh M, Yamaoka T;

XX WPI; 2001-193144/20.

XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.

XX Disclosure; Page 15; 25pp; English.

XX This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease

XX Sequence 9 AA;

Query Match 92.5%; Score 37; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
| | | | |
Db 1 DFMIQGGD 8

RESULT 7

AAG68089

ID AAG68089 standard; peptide; 9 AA.

XX

AC AAG68089;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Antitumour peptide cyclophilin B 91-99.
 XX
 XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.
 XX
 XX Homo sapiens.
 OS
 XX JP2001245675-A.
 PN
 XX 11-SEP-2001.
 PD
 XX 25-DEC-2000; 2000JP-00393047.
 PF
 XX 28-DEC-1999; 99JP-00374322.
 PR
 XX (ITOY/) ITO Y.
 PA
 XX WPI; 2001-610076/70.
 DR
 XX New peptides for recognizing cancer cells with tumor specific cytotoxic T
 XX lymphocytes and for treating cancer.
 PT
 XX Claim 8; Page 2; 14pp; Japanese.
 PS
 XX The present invention describes peptides recognising cancer cells with
 XX tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
 CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 CC the above mentioned sequences; and (4) peptides with one or more deleted,
 CC substituted, added or inserted amino acid(s) of the above mentioned
 CC sequences, particularly those having recognising property due to HLA-
 CC A2402 binding CTL, especially having at least 5 amino acids, used for
 CC medicine, particularly anticancer agents, derived from antitumour
 CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 CC genes. The antitumour peptides have cytostatic activities. The peptides
 CC are used for the treatment of cancer. The peptides cause activation of
 CC CTL in cancer patients. The present sequence represents a peptide from
 CC the present invention
 XX
 SQ Sequence 9 AA;
 Query Match 92.5%; Score 37; DB 4; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DXMIQGGD 8
 | |||||
 Db 1 DFMIQGGD 8
 RESULT 8
 ABG79076
 ID ABG79076 standard; peptide; 9 AA.
 XX
 AC ABG79076;
 XX
 XX 15-NOV-2002 (first entry)
 DT
 XX Human Cyp-B class I HLA widely expressed antigen peptide #2.
 DE
 XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; IIL; human leukocyte antigen; HLA;
 KW cytostatic; human.

XX Homo sapiens.
 OS
 XX WO200264057-A2.
 PN
 XX 22-AUG-2002.
 PD
 XX 15-FEB-2002; 2002WO-US005212.
 PF
 XX 15-FEB-2001; 2001US-0268687P.
 PR
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA
 XX Wang R;
 PI
 XX WPI; 2002-627577/67.
 DR
 XX Novel composition for treating a disease in an animal, comprises an
 XX immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 PT
 XX Disclosure; Page 17; 61pp; English.
 PS
 XX The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, kidney cancer, adenocarcinoma,
 CC cancer, cervical cancer, bladder cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 92.5%; Score 37; DB 5; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 DXMIQGGD 8
 | |||||
 Db 1 DFMIQGGD 8
 RESULT 9
 ABR84374
 ID ABR84374 standard; peptide; 9 AA.
 XX
 AC ABR84374;
 XX
 XX 06-NOV-2003 (first entry)
 DT
 XX Human CypB HLA-A24 epitope, SEQ ID NO:24.
 DE
 XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 KW human; human leukocyte antigen; HLA-A24 epitope.
 KW

OS Homo sapiens.
 XX JP2002365286-A.
 PN
 XX
 XX 18-DEC-2002.
 PD
 XX 18-SEP-2001; 2001JP-00283413.
 PF
 XX
 XX 13-NOV-2000; 2000JP-00345094.
 PR
 XX
 XX (ITOY/) ITO Y.
 PA
 XX
 XX WPI; 2003-508315/48.
 DR
 XX
 XX
 XX A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX
 XX Example 8; Page 10; 18pp; Japanese.
 PS
 XX The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 92.5%; Score 37; DB 6; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
 | | | | |
 Db 1 DFMIQGGD 8

RESULT 10
 ADC17709
 ID ADC17709 standard; peptide; 9 AA.
 XX
 XX ADC17709;
 AC
 DT 18-DEC-2003 (first entry)
 DX
 DE Modified cyclophilin B protein amino acids 91-99.
 XX
 XX cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.
 XX
 XX Synthetic.
 OS
 XX WO2003020306-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002WO-JP008641.
 XX
 XX 29-AUG-2001; 2001JP-00260046.
 XX
 XX (ITOH/) ITOH K.
 PA
 XX Itoh K, Yamada A;
 PI
 XX WPI; 2003-300831/29.
 DR
 XX Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.
 XX
 XX Claim 8; SEQ ID NO 2; 49pp; Japanese.
 PS
 XX The invention relates to allergic reaction suppressors, comprising a

XX WPI; 2003-300831/29.
 DR
 XX Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.
 XX
 XX Claim 8; SEQ ID NO 9; 49pp; Japanese.
 PS
 XX The invention relates to allergic reaction suppressors, comprising a
 CC peptide which originates from the same antigenic substance as the
 CC antigenic substance inducing the (peptide-originated) allergic reaction,
 CC and containing an epitope different from the epitope participating in the
 CC induction of the allergic reaction and yet does not induce the allergic
 CC reaction. The desensitizers or allergic reaction suppressors are useful
 CC for treating and preventing type I allergic diseases and in cancer
 CC vaccines for preventing or treating cancer. The allergic reaction
 CC suppressors are also useful for suppressing an allergic reaction or
 CC reducing immunoglobulin E antibody production, and for desensitization to
 CC antigens. This sequence represents a peptide used in the invention and
 CC corresponds to amino acids 91-99 of the cyclophilin B protein with the
 CC Phe at position 92 replaced by a Tyr.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 92.5%; Score 37; DB 7; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
 | | | | |
 Db 1 DFMIQGGD 8

RESULT 11
 ADC17702
 ID ADC17702 standard; peptide; 9 AA.
 XX
 XX ADC17702;
 AC
 DT 18-DEC-2003 (first entry)
 DX
 DE Cyclophilin B protein amino acids 91-99.
 XX
 XX cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.
 XX
 XX Synthetic.
 OS
 XX WO2003020306-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 28-AUG-2002; 2002WO-JP008641.
 XX
 XX 29-AUG-2001; 2001JP-00260046.
 XX
 XX (ITOH/) ITOH K.
 PA
 XX Itoh K, Yamada A;
 PI
 XX WPI; 2003-300831/29.
 DR
 XX Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.
 XX
 XX Claim 8; SEQ ID NO 2; 49pp; Japanese.
 PS
 XX The invention relates to allergic reaction suppressors, comprising a

CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet does not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 91-99 of the cyclophilin B protein.
XX
SQ Sequence 9 AA;

Query Match 92.5%; Score 37; DB 7; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| | | | |
Db 1 DFMIQGGD 8

RESULT 12
ADG89642
ID ADG89642 standard; peptide; 9 AA.

AC ADG89642;

XX 11-MAR-2004 (first entry)

XX Class I HLA-restricted widely expressed antigen #7.

XX metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; widely antigen.
XX

OS Unidentified.

XX WO2003100027-A2.

XX 04-DEC-2003.

XX 28-MAY-2003; 2003WO-US016736.

XX 28-MAY-2002; 2002US-0383530P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2004-035134/03.

XX Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.

XX Disclosure; SEQ ID NO 85; 137pp; English.

XX The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted widely expressed
CC antigen.

XX Sequence 9 AA;

Query Match 92.5%; Score 37; DB 8; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DXMIQGGD 8
| | | | |

Db 1 DFMIQGGD 8

RESULT 13

AAV69957

ID AAV69957 standard; peptide; 9 AA.

XX AAV69957;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #37.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.

XX Claim 4; Page 61; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match 67.5%; Score 27; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MIOGGD 8
| | | | |
Db 3 MCQGGD 8

RESULT 14

AAB12089

ID AAB12089 standard; peptide; 8 AA.

XX AAB12089;

XX 12-SEP-2003 (revised)

XX 17-JAN-2001 (first entry)

XX Ad7 cel peptide.

XX Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;

XX cell proliferation; cell differentiation; tissue repair;

XX transcription regulator; breast cancer; gene therapy; melanoma;

XX neuroblastoma; leukaemia; Parkinson's disease; Huntington's disease;

XX Alzheimer's disease; paralysis; motor neurone disorder; cel.

XX unidentified adenovirus.

PN US0609231-A.
 XX 30-MAY-2000.
 XX 18-AUG-1995; 95US-00516859.
 PF 18-AUG-1994; 94US-00292683.
 PR 06-MAR-1995; 95US-00399411.
 XX (LJOL-) LA JOLLA CANCER RES FOUND.
 XX Huang S;
 PI WPI; 2000-410879/35.
 XX
 XX New PR domain peptides comprising amino acid sequences from, for example
 PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for
 PT regulating gene transcription and controlling cell proliferation and
 PT differentiation.
 XX
 PS Disclosure; Fig 2; 91pp; English.
 XX
 CC The present sequence is Ad7 cel from Adenovirus. The cel domain is also
 CC found in rat retinoblastoma (Rb)-interacting zinc finger (RIZ) protein
 CC (AAB12028). RIZ is a nuclear phosphoprotein that acts as a cell
 CC differentiation factor. RIZ can modulate cell growth by binding to Rb
 CC protein, which is involved in regulating cell proliferation. In addition,
 CC RIZ can act to regulate transcription. RIZ functions to maintain cells in
 CC the G1 phase of the cell cycle, by interacting with Rb through the cr2
 CC domain of RIZ. Rat RIZ protein contains a number of GTPase motifs (see
 CC AAB12037 to AAB12056 and AAB12099 to AAB12104). RIZ protein is a PR
 CC domain protein and is present primarily in the cell nucleus. RIZ gene
 CC mutations may be implicated in various cancers such as melanoma,
 CC neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be
 CC used in gene therapy for these disorders. Since RIZ protein is implicated
 CC in cell cycle arrest, inhibition of RIZ activity may be useful in
 CC neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's or
 CC Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
 CC disorders e.g. heart disease, where the ability to induce neural/cardiac
 CC tissue proliferation would be useful. The present sequence was used for
 CC sequence homology comparison. (Updated on 12-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 8 AA;
 Query Match 62.5%; Score 25; DB 3; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.7e+06;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DXMIQGGD 8
 : : : : :
 Db 1 EDLLEGGD 8
 RESULT 15
 ADE84662
 ID ADE84662 standard; peptide; 8 AA.
 XX
 AC ADE84662;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Adenovirus 7 E1A gene cel domain.
 XX
 KW cytostatic; tumor; gene therapy;
 KW retinoblastoma protein-interacting zinc protein; RIZ; neuroblastoma;
 KW melanoma; cardiac cell growth inducer; neuronal cell growth inducer;
 KW adenovirus; E1A; cel.
 XX
 OS unidentified adenovirus.
 XX
 PN US6468985-B1.
 XX

PD 22-OCT-2002.
 XX 17-MAR-2000; 2000US-00528706.
 XX 18-AUG-1994; 94US-00292683.
 PR 06-MAR-1995; 95US-00399411.
 PR 18-AUG-1995; 95US-00516859.
 XX (BURN-) BURNHAM INST.
 PA
 XX Huang S;
 PI WPI; 2003-147106/14.
 DR
 XX
 XX Reducing the growth of tumor cell having mammalian retinoblastoma protein
 PT -interacting zinc finger proteins in a subject, comprises administering
 PT nucleic acid molecule encoding RIZ at or adjacent to the site of tumor.
 XX
 PS Example 3; SEQ ID NO 75; 49pp; English.
 XX
 CC The invention describes a method of reducing growth of a tumour cell
 CC having a mutant mammalian retinoblastoma (RB) protein-interacting zinc
 CC finger (RIZ) protein in a subject. The method comprises administering a
 CC nucleic acid molecule (I) encoding RIZ at or adjacent to tumour site. (I)
 CC is administered at the site of the tumour. The method is useful for
 CC reducing the growth of a tumour cell e.g. neuroblastoma or melanoma cell
 CC having mutant RIZ protein. The method is useful for inducing growth of a
 CC cardiac cell or a neuronal cell in a subject, and for effecting normal
 CC growth control to a tumour cell or causing differentiation of tumour
 CC cells. This is the amino acid sequence of an adenovirus cr1 domain used
 CC in a comparison with the cel domain of RIZ protein.
 XX
 SQ Sequence 8 AA;
 Query Match 62.5%; Score 25; DB 7; Length 8;
 Best Local Similarity 37.5%; Pred. No. 1.7e+06;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DXMIQGGD 8
 : : : : :
 Db 1 EDLLEGGD 8
 Search completed: October 21, 2004, 07:21:01
 Job time : 86 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGDX 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	62.5	8	2	US-08-459-568-75 Sequence 75, Appl
2	25	62.5	8	2	US-08-399-411-75 Sequence 75, Appl
3	25	62.5	8	3	US-08-516-859A-75 Sequence 75, Appl
4	25	62.5	8	3	US-09-586-472-75 Sequence 75, Appl
5	25	62.5	8	4	US-09-528-706-75 Sequence 75, Appl
6	25	62.5	9	1	US-08-457-172-1 Sequence 1, Appl
7	23	57.5	8	1	US-08-487-860-62 Sequence 62, Appl
8	23	57.5	11	3	US-08-953-327-1 Sequence 1, Appl
9	23	57.5	11	3	US-09-472-579-1 Sequence 1, Appl
10	22	55.0	9	1	US-08-215-805A-7 Sequence 7, Appl
11	22	55.0	9	1	US-08-215-805A-52 Sequence 52, Appl
12	22	55.0	9	1	US-08-215-805A-58 Sequence 58, Appl
13	21	52.5	10	3	US-09-296-284-10 Sequence 10, Appl
14	21	52.5	11	1	US-07-620-426B-19 Sequence 19, Appl
15	21	52.5	11	1	US-07-662-007B-19 Sequence 19, Appl
16	21	52.5	11	1	US-07-824-247-19 Sequence 19, Appl
17	21	52.5	11	3	US-08-470-204A-19 Sequence 19, Appl
18	20	50.0	9	1	US-08-215-805A-48 Sequence 48, Appl
19	20	50.0	9	1	US-08-215-805A-61 Sequence 61, Appl
20	20	50.0	9	1	US-08-215-805A-74 Sequence 74, Appl
21	20	50.0	9	3	US-09-139-802-84 Sequence 84, Appl
22	20	50.0	9	4	US-09-659-786-84 Sequence 84, Appl
23	20	50.0	9	4	US-08-926-914-84 Sequence 84, Appl
24	20	50.0	10	6	5196404-18 Patent No. 5196404
25	20	50.0	10	6	5433940-25 Patent No. 5433940
26	20	50.0	12	1	US-08-633-779-3 Sequence 3, Appl
27	20	50.0	12	1	US-08-633-779-5 Sequence 5, Appl

28	20	50.0	12	4	US-09-846-350A-1 Sequence 1, Appl
29	20	50.0	12	4	US-09-569-037-1 Sequence 1, Appl
30	20	50.0	12	4	US-09-569-037-15 Sequence 15, Appl
31	19	47.5	4	1	US-08-329-820-227 Sequence 227, App
32	19	47.5	6	1	US-08-329-820-101 Sequence 101, App
33	19	47.5	6	1	US-08-742-256-13 Sequence 13, Appl
34	19	47.5	6	4	US-09-113-696B-13 Sequence 13, Appl
35	19	47.5	6	6	RE34606-25 Patent No. RE34,60
36	19	47.5	7	1	US-07-940-861-39 Sequence 39, Appl
37	19	47.5	7	1	US-08-459-512-39 Sequence 39, Appl
38	19	47.5	7	1	US-08-798-897-27 Sequence 27, Appl
39	19	47.5	7	2	US-08-244-496-70 Sequence 70, Appl
40	19	47.5	7	2	US-08-978-523-27 Sequence 27, Appl
41	19	47.5	7	2	US-08-459-657-39 Sequence 39, Appl
42	19	47.5	7	2	US-08-460-132-39 Sequence 39, Appl
43	19	47.5	7	5	PCT-US92-02050-39 Sequence 39, Appl
44	19	47.5	8	2	US-08-286-819A-36 Sequence 36, Appl
45	19	47.5	8	3	US-08-980-357-36 Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-459-568-75
; Sequence 75, Application US/08459568
; Patent No. 5811104
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/459,568
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-75

Query Match 62.5%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8

Db 1 EDLLEGGD 8

RESULT 2
US-08-399-411-75
; Sequence 75, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-75

Query Match 62.5%; Score 25; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.Be+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIOGSD 8
; : : : : :
Db 1 EDLLEGGD 8

RESULT 3
US-08-516-859A-75
; Sequence 75, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995

CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-516-859A-75

Query Match 62.5%; Score 25; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIOGSD 8
; : : : : :
Db 1 EDLLEGGD 8

RESULT 4
US-09-586-472-75
; Sequence 75, Application US/09586472
; Patent No. 6323335
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/586,472
; FILING DATE: 01-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-586-472-75
Query Match 62.5%; Score 25; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
DB 1 EDLLEGGD 8

RESULT 5
US-09-528-706-75
; Sequence 75, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,663
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-528-706-75
Query Match 62.5%; Score 25; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3.8e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
DB 1 EDLLEGGD 8

RESULT 6
US-08-457-172-1
; Sequence 1, Application US/08457172
; Patent No. 5622837
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Hans Scheefers, Ursula Scheefers-Borchel and
; APPLICANT: Andreas Sziegoleit
; TITLE OF INVENTION: PANCREAS ELASTASE 1-SPECIFIC ANTIBODY, A PROCESS FOR
; TITLE OF INVENTION: OBTAINING IT, AND A TEST KIT CONTAINING SUCH ANTIBODY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,172
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,395
; FILING DATE:
; APPLICATION NUMBER: US 07/969,173
; FILING DATE: 29-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42883/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: pancreatic
US-08-457-172-1
Query Match 62.5%; Score 25; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGGD 8
DB 2 MVAGGD 7

RESULT 7
US-08-487-860-62
; Sequence 62, Application US/08487860
; Patent No. 5792456
; GENERAL INFORMATION:
; APPLICANT: Yelton, Dale
; APPLICANT: Glaser, Scott
; APPLICANT: Huse, William
; APPLICANT: Rosok, Mae J.
; TITLE OF INVENTION: No. 5792456el Mutant BR96 Antibodies and
; TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
```

RESULT 10
US-08-215-805A-7

```
; Sequence 7, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,805A
; FILING DATE: 22-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-215-805A-52

Query Match 55.0%; Score 22; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 IQGGD 8
DB 1 IDGGD 5

RESULT 11
US-08-215-805A-52
; Sequence 52, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,805A
; FILING DATE: 22-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Pasteurella suis
; STRAIN: 5943
; IMMEDIATE SOURCE:
; LIBRARY: P. suis DNA in Bacteriophage lambda-dash
; CLONE: (Lambda) yfG33-37
; US-08-215-805A-7

Query Match 55.0%; Score 22; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGGD 8
DB 1 IDGGD 5

RESULT 12
US-08-215-805A-58
; Sequence 58, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/215,805A
; FILING DATE: 22-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
```

```
; ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-803A-58

Query Match      55.0%; Score 22; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGG 8
Db 1 IHGD 5

RESULT 13
US-09-296-284-10
; Sequence 10, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Choi, Eun-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-10

Query Match      52.5%; Score 21; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DXMIQGG 7
Db 4 DALIQRG 10

RESULT 14
US-07-620-426B-19
; Sequence 19, Application US/07620426B
; Patent No. 5298421
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Maelor
; APPLICANT: Pollard, Michael Roman
; APPLICANT: Voekler, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/620,426B
; FILING DATE: 19901130
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: CGNE 70-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-620-426B-19

Query Match      52.5%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IQGG 7
Db 3 IQGG 6

RESULT 15
US-07-662-007B-19
; Sequence 19, Application US/07662007B
; Patent No. 5344771
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Maelor
; APPLICANT: Pollard, Michael Roman
; APPLICANT: Voekler, Toni Alois
; APPLICANT: Thompson, Gregory A.
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,007B
; FILING DATE: 19910408
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: CGNE 70-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-662-007B-19

Query Match      52.5%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 IQGG 7

Db 3 IQGG 6

Search completed: October 21, 2004, 07:29:29
Job time : 22.5 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGGD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	92.5	9	15	US-10-447-161-85
2	37	92.5	9	16	US-10-788-016-2
3	37	92.5	9	16	US-10-788-016-9
4	22	58.0	12	16	US-10-128-520-96
5	21	52.5	9	14	US-10-210-148-9
6	21	52.5	9	14	US-10-210-148-14
7	21	52.5	11	14	US-10-194-995-32
8	21	52.5	11	15	US-10-356-257-161
9	20	50.0	5	14	US-10-076-047A-124
10	20	50.0	5	16	US-10-620-052A-50
11	20	50.0	9	9	US-09-765-086-84
12	20	50.0	9	9	US-09-912-787-35
13	20	50.0	9	13	US-10-014-326-21
14	20	50.0	9	14	US-10-264-374-84

15	20	50.0	9	14	US-10-375-992-84	Sequence 84, Appl
16	20	50.0	9	14	US-10-137-867-10	Sequence 10, Appl
17	20	50.0	9	15	US-10-264-374-84	Sequence 84, Appl
18	20	50.0	9	16	US-10-375-992-84	Sequence 84, Appl
19	20	50.0	10	9	US-09-846-350-1	Sequence 1, Appl
20	20	50.0	11	9	US-09-846-342-1	Sequence 1, Appl
21	20	50.0	12	9	US-09-845-725-1	Sequence 1, Appl
22	20	50.0	12	14	US-10-148-687-32	Sequence 32, Appl
23	19	47.5	4	14	US-10-084-388A-2	Sequence 2, Appl
24	19	47.5	5	14	US-10-076-047A-130	Sequence 130, Appl
25	19	47.5	5	15	US-10-436-549-36	Sequence 36, Appl
26	19	47.5	5	16	US-10-712-425-36	Sequence 36, Appl
27	19	47.5	5	17	US-10-723-933-96	Sequence 96, Appl
28	19	47.5	6	9	US-09-113-696B-13	Sequence 13, Appl
29	19	47.5	6	17	US-10-723-933-25	Sequence 25, Appl
30	19	47.5	6	17	US-10-723-933-97	Sequence 97, Appl
31	19	47.5	6	17	US-10-723-933-120	Sequence 120, Appl
32	19	47.5	7	14	US-10-190-082-84	Sequence 84, Appl
33	19	47.5	7	14	US-10-190-082-159	Sequence 159, Appl
34	19	47.5	7	16	US-10-481-180-426	Sequence 426, Appl
35	19	47.5	7	17	US-10-723-933-7	Sequence 7, Appl
36	19	47.5	7	17	US-10-723-933-12	Sequence 12, Appl
37	19	47.5	7	17	US-10-723-933-26	Sequence 26, Appl
38	19	47.5	7	17	US-10-723-933-88	Sequence 88, Appl
39	19	47.5	7	17	US-10-723-933-98	Sequence 98, Appl
40	19	47.5	8	15	US-10-462-452-445	Sequence 445, Appl
41	19	47.5	8	15	US-10-601-953-574	Sequence 574, Appl
42	19	47.5	8	16	US-10-322-266-446	Sequence 446, Appl
43	19	47.5	8	17	US-10-723-933-11	Sequence 11, Appl
44	19	47.5	8	17	US-10-723-933-27	Sequence 27, Appl
45	19	47.5	8	17	US-10-723-933-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-447-161-85
; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match 92.5%; Score 37; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
Db 1 DFMIQGGD 8

RESULT 2
US-10-788-016-2
; Sequence 2, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto

;; TITLE OF INVENTION: Desensitizers
;; FILE REFERENCE: 3190-049
;; CURRENT APPLICATION NUMBER: US/10/788,016
;; CURRENT FILING DATE: 2004-02-26
;; PRIOR APPLICATION NUMBER: PCT/JP02/08641
;; PRIOR FILING DATE: 2002-08-28
;; PRIOR APPLICATION NUMBER: JP P2001-260046
;; PRIOR FILING DATE: 2001-08-29

;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 2
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial

;; FEATURE:
;; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
;; OTHER INFORMATION: to the 99th residue of cyclophilin B
US-10-788-016-2

Query Match 92.5%; Score 37; DB 16; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
Db 1 DFMIQGGD 8

RESULT 3

US-10-788-016-9
;; Sequence 9, Application US/10788016
;; Publication No. US20040141992A1

;; GENERAL INFORMATION:

;; APPLICANT: ITOH, Kyogo
;; TITLE OF INVENTION: Desensitizers
;; FILE REFERENCE: 3190-049
;; CURRENT APPLICATION NUMBER: US/10/788,016
;; CURRENT FILING DATE: 2004-02-26
;; PRIOR APPLICATION NUMBER: PCT/JP02/08641
;; PRIOR FILING DATE: 2002-08-28
;; PRIOR APPLICATION NUMBER: JP P2001-260046
;; PRIOR FILING DATE: 2001-08-29

;; NUMBER OF SEQ ID NOS: 9

;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 9
;; LENGTH: 9
;; TYPE: PRT

;; ORGANISM: Artificial

;; FEATURE:
;; OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
;; OTHER INFORMATION: residues from the 91st residue to the 99th residue of
;; OTHER INFORMATION: cyclophilin B
US-10-788-016-9

Query Match 92.5%; Score 37; DB 16; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
Db 1 DYMIQGGD 8

RESULT 4

US-10-128-520-96
;; Sequence 96, Application US/10128520
;; Publication No. US20040105862A1

;; GENERAL INFORMATION:

;; APPLICANT: PAN et al.
;; TITLE OF INVENTION: Human TIMP-1 Antibodies
;; FILE REFERENCE: 02973-00073
;; CURRENT APPLICATION NUMBER: US/10/128,520
;; CURRENT FILING DATE: 2002-04-24

;; PRIOR APPLICATION NUMBER: US 60/285,683
;; PRIOR FILING DATE: 2001-04-24

;; NUMBER OF SEQ ID NOS: 381

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 96

;; LENGTH: 12

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-128-520-96

Query Match 55.0%; Score 22; DB 16; Length 12;
Best Local Similarity 37.5%; Pred. No. 9.7e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DXMIQGGD 8
Db 5 DQLQGGSE 12

RESULT 5

US-10-210-148-9

;; Sequence 9, Application US/10210148

;; Publication No. US20030171280A1

;; GENERAL INFORMATION:

;; APPLICANT: Soderstrom, Karl Petter

;; TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response

;; FILE REFERENCE: TROM0002

;; CURRENT APPLICATION NUMBER: US/10/210,148

;; CURRENT FILING DATE: 2002-07-31

;; PRIOR APPLICATION NUMBER: PCT/US02/24311

;; PRIOR FILING DATE: 2002-07-31

;; NUMBER OF SEQ ID NOS: 117

;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 9

;; LENGTH: 9

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-210-148-9

Query Match 52.5%; Score 21; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGGD 8
Db 2 MIOGGD 7

RESULT 6

US-10-210-148-14

;; Sequence 14, Application US/10210148

;; Publication No. US20030171280A1

;; GENERAL INFORMATION:

;; APPLICANT: Soderstrom, Karl Petter

;; TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response

;; FILE REFERENCE: TROM0002

;; CURRENT APPLICATION NUMBER: US/10/210,148

;; CURRENT FILING DATE: 2002-07-31

;; PRIOR APPLICATION NUMBER: PCT/US02/24311

;; PRIOR FILING DATE: 2002-07-31

;; NUMBER OF SEQ ID NOS: 117

;; SOFTWARE: PatentIn version 3.2

;; SEQ ID NO 14

;; LENGTH: 9

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-210-148-14

Query Match 52.5%; Score 21; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGGD 8

Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadib, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-09-765-086-84

Query Match 50.0%; Score 20; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGG 8
|: ||
Db 3 MVRDGD 8

RESULT 12

US-09-912-787-35
; Sequence 35, Application US/09912787
; Publication No. US20020119149A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBSEN, Bent Karsten
; APPLICANT: BOULTER, Jonathan Michael
; TITLE OF INVENTION: Multivalent T Cell Receptor Complexes
; FILE REFERENCE: 102286.410DIV
; CURRENT APPLICATION NUMBER: US/09/912.787
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 09/334,969
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/GB99 01583
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: GB 9810759.2
; PRIOR FILING DATE: 1998-05-19
; PRIOR APPLICATION NUMBER: GB 9821129.5
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: New
; OTHER INFORMATION: N-terminal amino acid sequence of the truncated
; OTHER INFORMATION: Vbeta17 chain of the human JM22 Influenza Matrix
; OTHER INFORMATION: peptide/HLA-A0201 restricted TCR.
US-09-912-787-35

Query Match 50.0%; Score 20; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGG 7
|: ||
Db 1 MVDGG 5

RESULT 13

US-10-014-326-21
; Sequence 21, Application US/10014326
; Publication No. US20020142389A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBSEN, Bent Karsten
; APPLICANT: BELL, John Irving
; APPLICANT: GAO, George Fu
; APPLICANT: WILCOX, Benjamin Ernest
; APPLICANT: BOULTER, Jonathan Michael
; TITLE OF INVENTION: Soluble T Cell Receptor
; FILE REFERENCE: 102286.409
; CURRENT APPLICATION NUMBER: US/10/014,326
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/335,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB/9810759.2
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: New N-terminal amino acid sequence of truncated V
; OTHER INFORMATION: beta17 chain of the human JM22 Influenza matrix
; OTHER INFORMATION: peptide/HLA-A0201 restricted TCR. (Figure 9B).
; OTHER INFORMATION: Description of Artificial Sequence: New N-terminal
; OTHER INFORMATION: amino acid sequence of truncated V beta17 chain of
; OTHER INFORMATION: the JM22 Influenza matrix peptide/HLA-A0201
; OTHER INFORMATION: restricted TCR. (Figure 9A)
US-10-014-326-21

Query Match 50.0%; Score 20; DB 13; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGG 7
|: ||
Db 1 MVDGG 5

RESULT 14

US-10-264-374-84
; Sequence 84, Application US/10264374
; Publication No. US20030113320A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/10/264,374
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US/09/139,802
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 08/926,914
; PRIOR FILING DATE: 1997-09-10
; PRIOR APPLICATION NUMBER: 08/710,067
; PRIOR FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-264-374-84

Query Match 50.0%; Score 20; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGD 8
|::||
Db 3 MYRGG 8

RESULT 15

US-10-375-992-84
; Sequence 84, Application US/10375992
; Publication No. US20030152578A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; Pasqualini, Renata
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
; Derived Therefrom, and Methods of Using Same
; NUMBER OF SEQUENCES: 199
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/10/375,992
; APPLICATION NUMBER: US/10/375,992
; FILING DATE: 27-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,914
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2725
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-375-992-84

Query Match 50.0%; Score 20; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGD 8
|::||
Db 3 MYRGG 8

Search completed: October 21, 2004, 07:33:42
Job time : 62.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 : Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-38

Perfect score: 40

Sequence: 1 DXMIQGGDX 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	50.0	12	S43170	kinesin light chain
2	19	47.5	11	B60769	Ig H2 chain - Pacific hagfish (fragment)
3	18	45.0	7	PT0542	T-cell receptor beta
4	18	45.0	9	QDRB	delta sleep-inducible
5	18	45.0	11	PH1343	Ig heavy chain DJ
6	18	45.0	11	S60354	retinal oxidase -
7	18	45.0	11	PN0044	protein kinase C i
8	18	45.0	11	PT0218	T-cell receptor beta
9	18	45.0	11	I41946	T-cell receptor gamma
10	18	45.0	11	A61575	Trimeresurus serin
11	17	42.5	3	A23751	spinal cord peptid
12	17	42.5	3	YFPG	thymic factor - pi
13	17	42.5	9	A60957	thymocyte growth p
14	17	42.5	11	S57575	T cell receptor V-
15	17	42.5	11	D37196	bradykinin-potent
16	17	42.5	11	S19015	hypothetical prote
17	17	42.5	12	PH1458	T-cell receptor be
18	16	40.0	12	A61309	glycoprotein hormo
19	16	40.0	12	S65730	hemoglobin, extrac
20	16	40.0	12	T46794	hypothetical prote
21	15	37.5	4	S47552	ubiquitin - rat
22	15	37.5	4	S09478	globulin IV alpha
23	15	37.5	7	S58797	serine/threonine-s
24	15	37.5	7	S15597	orf 4 rara 5'-regi
25	15	37.5	8	A31570	angiotensin-conver
26	15	37.5	9	I50633	c-rel protein - ch
27	15	37.5	10	PC2172	triacylglycerol li
28	15	37.5	10	PT0309	Ig heavy chain CRD
29	15	37.5	10	B56899	serum heterodimer,

30	15	37.5	11	2	A38590	transforming prote
31	15	37.5	12	2	S26544	T-cell receptor be
32	15	37.5	12	2	PA0030	protein QA300025 -
33	15	37.5	12	2	E44787	callimuramide 1 -
34	15	37.5	12	2	A53252	pollen major aller
35	14	35.0	5	2	B61168	cocoonase (EC 3.4.
36	14	35.0	5	2	I50385	myosin light chain
37	14	35.0	7	2	E61491	seed protein ws-5
38	14	35.0	7	2	PT0667	T-cell receptor be
39	14	35.0	7	2	PT0586	T-cell receptor be
40	14	35.0	7	2	T09512	NADH2 dehydrogenas
41	14	35.0	8	2	C39690	neural cell adhesi
42	14	35.0	9	2	S66608	quinoline 2-oxidor
43	14	35.0	9	2	A53797	3', 5'-cyclic-GMP p
44	14	35.0	9	2	A57444	neuropeptide Grb-A
45	14	35.0	9	2	B57444	neuropeptide Grb-A

ALIGNMENTS

RESULT 1

S43170
kinesin light chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: S43170
R:Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
submitted to the EMBL Data Library, December 1992
A:Description: Promoter first exon/intron characterization and chromosomal location of th
A:Reference number: S43170
A:Accession: S43170
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <CHE>
A:Cross-references: UNIPROT:Q13865; EMBL:X69658; NID:g468786; PIDN:CRA49349.1; PID:g468786

Query Match 50.0%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIQGG 7
|::||
Db 1 MLRGG 5

RESULT 2

B60769
Ig H2 chain - Pacific hagfish (fragment)
C:Species: Eptatretus stouti (Pacific hagfish)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C:Accession: B60769
R:Hanley, P.O.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A>Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A:Reference number: A60769; MUID:91060965; PMID:2123225
A:Accession: B60769
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HAN>

Query Match 47.5%; Score 19; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DXMIQ 5
|::||
Db 5 DFMIQ 9

RESULT 3

PT0542
T-cell receptor beta chain V-D-J region (126-1BA) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0542
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0542
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <PEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
DB 3 GGD 5

RESULT 4

QDRB
delta sleep-inducing peptide - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C;Accession: A01422
R;Monnier, M.; Dudley, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.
Experientia 33, 548-552, 1977
A;Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original
A;Reference number: A01422; MUID:77185324; PMID:862769
A;Accession: A01422
A;Molecule type: protein
A;Residues: 1-9 <MON>
A;Cross-references: UNIPROT:P01158
C;Comment: This peptide was obtained from dialysates of occipital venous sinus blood from
of recipient rabbits, it induces spindle and delta EEG activity and reduced motor activity

Query Match 45.0%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
DB 3 GGD 5

RESULT 5

PH1343
Ig heavy chain DJ region (clone C100-91) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1343
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1343
A;Molecule type: DNA
A;Residues: 1-11 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
DB 1 GGD 3

RESULT 6

S60354
retinal oxidase - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S60354
R;Huang, D.Y.; Ichikawa, Y.
Biochim. Biophys. Acta 1243, 431-436, 1995
A;Title: Identification of essential lysyl and cysteinyl residues, and the amino acid sequence
A;Reference number: S60354; MUID:95244596; PMID:77727518
A;Accession: S60354
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HUA>

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
DB 1 GGD 3

RESULT 7

PN0044
protein kinase C inhibitor I - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0044
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma
A;Reference number: PN0041
A;Accession: PN0044
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocked
C;Keywords: brain

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
DB 8 GGD 10

RESULT 8

PT0218
T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0218
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0218
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGGD 8
|||
DB 5 QGGN 8

RESULT 9

I41946
T-cell receptor gamma chain (St.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: I41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:920493116; PMID:1658619
A:Accession: I41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <WHE>
C:Keywords: T-cell receptor

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 5 GGD 7

RESULT 10

A61575
Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)
N:Alternate names: hemorrhagic toxin
C:Species: Trimeresurus elegans (Sakishima habu)
C:Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: A61575
R:Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.
Int. J. Biochem. 23, 73-78, 1991
A:Title: Isolation and characterization of hemorrhagic toxin from the venom of Trimeresurus
A:Reference number: A61575; MUID:91216327; PMID:2022298
A:Accession: A61575
A:Molecule type: protein
A:Residues: 1-11 <NIK>
C:Keywords: hydrolase; serine proteinase; venom

Query Match 45.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 3 GGD 5

RESULT 11

A23751
spinal cord peptide SCP-4 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: A23751
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <HSI>

Query Match 42.5%; Score 17; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
|||
Db 1 QGG 3

RESULT 12

YFP6
thymic factor - pig
N:Alternate names: FTS (facteur thymique serique)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C:Accession: A01523; A60983
R:Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A:Title: Structural study of circulating thymic factor: a peptide isolated from pig serum
A:Reference number: A01523; MUID:78026571; PMID:914862
A:Accession: A01523
A:Molecule type: protein
A:Residues: 1-9 <PLE>
A:Cross-references: UNIPROT:P01255
R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A:Title: Biochemical characterisation of a serum thymic factor.
A:Reference number: A60983; MUID:77123829; PMID:300146
A:Accession: A60983
A:Molecule type: protein
A:Residues: 'Z', '2-4', 'Z', '6-9 <BAC>
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modification
C:Superfamily: thymic factor
C:Keywords: pyroglutamic acid
F:/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 42.5%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
|||
Db 5 QGG 7

RESULT 13

A60957
thymocyte growth peptide - sheep
N:Contains: FTS (facteur thymique serique)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A60957
R:Ernstroem, U.; Gaivelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship t
A:Reference number: A60957; MUID:91064427; PMID:2249604
A:Accession: A60957
A:Molecule type: protein
A:Residues: 1-9 <ERN>
A:Cross-references: UNIPROT:Q7M3C5
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C:Comment: This peptide was isolated in two forms. One form contained the pyroglutamate carboxylamide (Glx) (in FTS) #status experimental
F:/Modified site: pyroglutamate carboxylamide (Glx) (in thymocyte growth peptide) #status experimental

Query Match 42.5%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
|||
Db 5 QGG 7

RESULT 14

S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57575
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A;Reference number: S57494
A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11 <BUR>
A;Cross-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor

Query Match 42.5%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
Db 4 QGG 6

RESULT 15
D37196
bradykinin-potentiating peptide 4 - island jaxaraca
C;Species: Bothrops insularis (island jaxaraca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: D37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: D37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CIN>
A;Cross-references: UNIPROT:P30424
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.5%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QGG 7
Db 1 QGG 3

Search completed: October 21, 2004, 07:27:58
Job time : 16.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-38
Perfect score: 40
Sequence: 1 DXMIQGDGX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	57.5	7	2 Q63480	Q63480 rattus norv
2	22	55.0	12	2 Q9H3W2	Q9H3W2 homo sapien
3	21	52.5	12	2 Q70Y58	Q70Y58 clinopodium
4	21	52.5	12	2 CAD45546	CAD45546 clinopodi
5	20	50.0	12	2 Q13865	Q13865 homo sapien
6	19	47.5	7	2 Q70Y98	Q70Y98 rattus norv
7	19	47.5	11	2 Q70Y98	Q70Y98 capitanopei
8	19	47.5	11	2 CAD45456	CAD45456 capitanopei
9	18	45.0	9	1 DSIP RABIT	P01158 oryctolagus
10	18	45.0	9	2 Q6LDH6	Q6LDH6 rattus norv
11	18	45.0	9	2 AAA40600	AAA40600 rattus no
12	18	45.0	10	2 Q51812	Q51812 plasmod f.
13	18	45.0	12	2 Q9H1Z6	Q9H1Z6 homo sapien
14	18	45.0	12	2 Q9N2B8	Q9N2B8 pongo pygma
15	18	45.0	12	2 Q9N2B9	Q9N2B9 gorilla gor
16	18	45.0	12	2 Q9N2C0	Q9N2C0 pan troglod
17	18	45.0	12	2 Q54226	Q54226 saccharopol
18	17	42.5	7	1 ASCL ALLAS	P84071 allium asca
19	17	42.5	9	1 THYF RIG	P01255 sus scrofa
20	17	42.5	9	2 Q7M3C5	Q7M3C5 ovine aries
21	17	42.5	10	2 Q6LC14	Q6LC14 homo sapien
22	17	42.5	10	2 Q96QA7	Q96QA7 homo sapien
23	17	42.5	10	2 AAD14854	AAD14854 homo sapi
24	17	42.5	11	1 BPP4_BOTIN	P30424 bothrops in
25	17	42.5	11	2 Q70Y64	Q70Y64 plectranthu
26	17	42.5	11	2 Q47420	Q47420 escherichia
27	17	42.5	11	2 CAD45529	CAD45529 plectrant
28	16	40.0	10	1 ESTA_SCHGA	P81012 schizaphis
29	16	40.0	10	2 Q8UUVW2	Q8UUVW2 oreochromis
30	16	40.0	12	2 Q7M0A7	Q7M0A7 cricetidae
31	16	40.0	12	2 Q8UUVV8	Q8UUVV8 squalus aca

```

32 16 40.0 12 2 Q8UUVW0 Q8UUVW0 rana catesb
33 15 37.5 8 1 ACI_THUAL P18691 thunnus alb
34 15 37.5 8 2 Q9F0K3 Q9F0K3 homo sapien
35 15 37.5 9 2 Q9BQT4 Q9BQT4 homo sapien
36 15 37.5 9 2 Q6YF34 Q6YF34 rattus norv
37 15 37.5 9 2 Q92C09 Q92C09 gallus gall
38 15 37.5 9 2 AAN87279 AAN87279 rattus no
39 15 37.5 10 2 Q6X2S9 Q6X2S9 homo sapien
40 15 37.5 10 2 Q85V66 Q85V66 eucalyptus
41 15 37.5 10 2 Q7LZJ7 Q7LZJ7 carcharhinu
42 15 37.5 10 2 Q7ZZJ2 Q7ZZJ2 motacilla f
43 15 37.5 10 2 AAP83315 AAP83315 homo sapi
44 15 37.5 11 2 Q7ZZI6 Q7ZZI6 motacilla f
45 15 37.5 11 2 Q7ZZI9 Q7ZZI9 motacilla f

```

ALIGNMENTS

```

RESULT 1
Q63480 PRELIMINARY; PRT; 7 AA.
ID Q63480;
AC Q63480;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
DR EMBL; U59125; AAB02827.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;
Query Match 57.5%; Score 23; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 IQGGD 8
DB 2 IRGGD 6
RESULT 2
Q9H3W2 PRELIMINARY; PRT; 12 AA.
ID Q9H3W2;
AC Q9H3W2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE TRE17 protein.
GN Name=TRE17 gene;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=94010310; PubMed=8406013;
RA Onno M., Nakamura T., Hillova J., Hill M.;

```


GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Deterra-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., DuPont B.R., Leach R.J., Deterra-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
Query Match 47.5%; Score 19; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 ICGGD 8
Db 2 ICGGD 6
RESULT 7
Q70Y98 PRELIMINARY; PRT; 11 AA.
ID Q70Y98;
AC Q70Y98;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Ribosomal protein (fragment).
GN Name=rp16;
OS Capitanopsis angustifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Capitanopsis.
OX NCBI_TaxID=204110;
RN [1]
RP SEQUENCE FROM N.A.
RC Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505333; CAD45456.1; -
KW Chloroplast; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 11 AA; 1161 MW; 2AB3C5D9BEAB5878 CRC64;
Query Match 47.5%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 MIQGG 7
Db 1 LFQGG 5

RESULT 8
CAD45456 PRELIMINARY; PRT; 11 AA.
ID CAD45456
AC CAD45456;
DT 14-MAR-2004 (TRENBLrel. 27, Created)
DT 14-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Ribosomal protein (fragment).
GN RPS16.
OS Capitanopsis angustifolia.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Capitanopsis.
OX NCBI_TaxID=204110;
RN [1]
RP SEQUENCE FROM N.A.
RC Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505333; CAD45456.1; -
KW Chloroplast; Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 11 AA; 1161 MW; 2AB3C5D9BEAB5878 CRC64;
Query Match 47.5%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 MIQGG 7
Db 1 LFQGG 5

RESULT 9
DSIP RABIT STANDARD; PRT; 9 AA.
ID DSIP RABIT
AC P01159;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Delta sleep-inducing peptide (DSIP).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=77185324; PubMed=862769;
RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
RA Schoenenberger G.A.;
RT "The delta sleep inducing peptide (DSIP). Comparative properties of
the original and synthetic nonapeptide.";
RL Experientia 33:548-552(1977).
RN [2]
RP SEQUENCE AND SYNTHESIS.
RX MEDLINE=79054421; PubMed=568769;
RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
analysis, sequence, synthesis and activity of the nonapeptide.";
RL Pflugers Arch. 376:119-129(1978).
RN [3]
RP REVIEW.
RX MEDLINE=87175129; PubMed=3550726;
RA Graf M.V., Kastin A.J.;
RT "Delta-sleep-inducing peptide (DSIP): an update.";

RP SEQUENCE FROM N.A.
RA Gonzalez-Gomez F., Vergara F., Pedrosa C., Ramirez J.P.,
RA Castilla J.A., Yoldi A., Ruiz A., Real L.M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326912; AAG42501.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1385 MW; 09168BCB76C41404 CRC64;

Query Match 45.0%; Score 18; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 9.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DXMIQGG 7
Db 4 DNRQGG 10

RESULT 14

Q9N2B8 PRELIMINARY; PRT; 12 AA.
AC Q9N2B8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041365; BAA94454.1; -;
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match 45.0%; Score 18; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
Db 7 GGD 9

RESULT 15

Q9N2B9 PRELIMINARY; PRT; 12 AA.
AC Q9N2B9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041364; BAA94453.1; -;
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

KW Methyltransferase; Transferase.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 45.0%; Score 18; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
Db 7 GGD 9

Search completed: October 21, 2004, 07:26:49
Job time : 88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	3 AAY69962	Aay69962 Human cyc
2	50	100.0	9	4 AAB46946	Aab46946 Human cyc
3	46	92.0	9	3 AAY69921	Aay69921 Human cyc
4	46	92.0	9	4 AAB46930	Aab46930 Human cyc
5	46	92.0	9	5 AAG68088	Aag68088 Antitumou
6	46	92.0	9	5 ABG79075	Abg79075 Human Cyp
7	46	92.0	9	6 ABR84373	Abx84373 Human Cyp
8	46	92.0	9	7 ADC17701	Adc17701 Cyclophil
9	46	92.0	9	8 ADG89641	Adg89641 Class I H
10	36	72.0	9	3 AAY69960	Aay69960 Human cyc
11	31	62.0	10	2 AAR96521	Aar96521 Hepatitis
12	31	62.0	11	4 AAB82292	Aab82292 Phosphory
13	29	58.0	9	3 AAY69959	Aay69959 Human cyc
14	29	58.0	11	3 AAY69924	Aay69924 Human cyc
15	28	56.0	9	5 ABG94771	Abg94771 Replikin
16	28	56.0	9	5 ABG94772	Abg94772 Replikin
17	28	56.0	9	6 ABUS7321	Abu57321 Replikin
18	28	56.0	9	6 ABUS7322	Abu57322 Replikin
19	28	56.0	9	7 ADD88394	Add88394 Tumour vi
20	28	56.0	9	7 ADD88395	Add88395 Tumour vi
21	28	56.0	9	7 ADG18172	Adg18172 Tumour vi
22	28	56.0	9	7 ADG18173	Adg18173 Tumour vi
23	28	56.0	12	8 ADI46367	Adi46367 Permeabil
24	27	54.0	9	5 AAU71498	Aau71498 Human MHC
25	27	54.0	9	5 AAU71218	Aau71218 Human MHC

ALIGNMENTS

RESULT 1
AAY69962
ID AAY69962 standard; peptide; 9 AA.

XX AC AAY69962;
XX AC
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #42.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.

XX OS
XX FN WO9967288-Al.
XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITOH/) ITOH K.
XX Itoh K, Gomi S;
XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX diagnosis of tumors.
XX Claim 10; Page 60; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B, that
XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYHRVIKDF 9

|||||||

Aau71556 Human MHC
Aau71745 Human MHC
Adm41409 Human bec
Aaw92359 CYP2B1 im
Aar48203 Human pho
Aab82291 Phosphory
Aab82294 Phosphory
Aap93365 Amino aci
Abp11571 HIV A01 s
Abp15315 HIV A24 s
Abp20150 HIV A03 m
Abp15417 HIV A24 s
Abp11625 HIV A01 s
Abp15505 HIV A24 s
Abp20151 HIV A03 m
Abp17665 HIV B58 s
Abp15503 HIV A24 s
Adp79463 Parapoxvi
Adp74879 Parapoxvi
Abr11047 Human can

26 27 54.0 10 5 AAU71556
27 27 54.0 10 5 AAU71745
28 27 54.0 10 8 ADM41409
29 27 54.0 12 2 AAW92359
30 26 52.0 11 2 AAR48203
31 26 52.0 11 4 AAB82291
32 26 52.0 11 4 AAB82294
33 26 52.0 12 1 AAP93365
34 25.5 51.0 9 4 ABP11571
35 25.5 51.0 9 4 ABP15315
36 25.5 51.0 10 4 ABP20150
37 25.5 51.0 10 4 ABP15417
38 25.5 51.0 11 4 ABP11625
39 25.5 51.0 11 4 ABP15505
40 25.5 51.0 11 4 ABP20151
41 25.5 51.0 11 4 ABP17665
42 25.5 51.0 11 4 ABP15503
43 25 50.0 7 7 ADP79463
44 25 50.0 7 8 ADP74879
45 25 50.0 9 6 ABR11047

Db 1 KYHRVIKDF 9

RESULT 2

AAB46946
ID AAB46946 standard; peptide; 9 AA.

XX AAB46946;

AC 04-MAY-2001 (first entry)

XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.

XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;

KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;

KW viral infectious disease; cyclophilin B; human.

XX Homo sapiens.

OS EPI074267-A1.

PN 07-FEB-2001.

XX 24-JUL-2000; 2000EP-00306263.

XX 22-JUL-1999; 99JP-00207687.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Takasu H, Gotoh M, Yamaoka T;

XX WPI; 2001-193144/20.

XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX Disclosure; Page 19; 25pp; English.

XX This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease

XX Sequence 9 AA;

Query Match 100.0%; Score 50; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYHRVIKDF 9

DB 1 KYHRVIKDF 9

RESULT 3

AAAY69921
ID AAAY69921 standard; peptide; 9 AA.

XX AAAY69921;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #1.

DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX HLA antigen; diagnosis; tumour; therapy.

KW Homo sapiens.

OS WO9967288-A1.

PN 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

XX diagnosis of tumors.

XX Claim 4; Page 49; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match 92.0%; Score 46; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.7e+06;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KYHRVIKDF 9

DB 1 KYHRVIKDF 9

RESULT 4

AAB46930
ID AAB46930 standard; peptide; 9 AA.

XX AAB46930;

XX 04-MAY-2001 (first entry)

XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 16.

XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;

XX virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;

XX viral infectious disease; cyclophilin B; human.

XX Homo sapiens.

OS EPI074267-A1.

PN 07-FEB-2001.

XX 24-JUL-2000; 2000EP-00306263.

XX 22-JUL-1999; 99JP-00207687.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX Takasu H, Gotoh M, Yamaoka T;

XX WPI; 2001-193144/20.

XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.
XX
PS Disclosure; Page 15; 25pp; English.
XX
CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cytostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease
XX
SQ Sequence 9 AA;
Query Match 92.0%; Score 46; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHRVIKDF 9
DB 1 KFHVRVIKDF 9
:|||||
:|||||
RESULT 5
AAG68088
ID AAG68088 standard; peptide; 9 AA.
XX
AC AAG68088;
XX
XX 17-DEC-2001 (first entry)
XX
DE Antitumour peptide cyclophilin B 84-92.
XX
XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
KW cyclophilin B gene; HLA-A2402.
XX
XX Homo sapiens.
OS
XX JP2001245675-A.
PN
XX 11-SEP-2001.
PD
XX 25-DEC-2000; 2000JP-00393047.
PF
XX 28-DEC-1999; 99JP-00374322.
PR
XX (ITOY/) ITO Y.
PA
XX WPI; 2001-610076/70.
DR
XX
XX New peptides for recognizing cancer cells with tumor specific cytotoxic T
PT lymphocytes and for treating cancer.
PT
XX
PS Claim 8; Page 2; 14pp; Japanese.
XX
CC The present invention describes peptides recognising cancer cells with
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
CC cancer cells with tumour specific CTLs are selected from: (1) peptides of
CC sequences (AAG68066 to AAG68069); (2) peptides containing the above
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with
CC the above mentioned sequences; and (4) peptides with one or more deleted,

CC substituted, added or inserted amino acid(s) of the above mentioned
CC sequences, particularly those having recognising property due to HLA-
CC A2402 binding CTL, especially having at least 5 amino acids, used for
CC medicine, particularly anticancer agents, derived from antitumour
CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
CC genes. The antitumour peptides have cytostatic activities. The peptides
CC are used for the treatment of cancer. The peptides cause activation of
CC CTL in cancer patients. The present sequence represents a peptide from
CC the present invention
XX
SQ Sequence 9 AA;
Query Match 92.0%; Score 46; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHRVIKDF 9
DB 1 KFHVRVIKDF 9
:|||||
:|||||
RESULT 6
ABG79075
ID ABG79075 standard; peptide; 9 AA.
XX
AC ABG79075;
XX
XX 15-NOV-2002 (first entry)
DT
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #1.
XX
XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
XX cytostatic; human.
XX
XX Homo sapiens.
OS
XX WO200264057-A2.
PN
XX 22-AUG-2002.
PD
XX 15-FEB-2002; 2002WO-US005212.
PF
XX 15-FEB-2001; 2001US-0268687P.
PR
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA
XX Wang R;
PI
XX WPI; 2002-627577/67.
DR
XX
XX Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (i), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (i) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (i), where antigen enters into the cell. The antigen-
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following

CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I), with,
CC preferably dendritic cell is prior to, subsequent to or concurrent
CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention

XX SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0;

QY 1 KYHRVIKDF 9
|:|||||
Db 1 KFHVRVIKDF 9

RESULT 7

ABR84373

ID ABR84373 standard; peptide; 9 AA.

XX AC ABR84373;

XX 06-NOV-2003 (first entry)

XX Human CypB HLA-A24 epitope, SEQ ID NO:23.

XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.

XX Homo sapiens.

XX JP2002365286-A.

XX 18-DEC-2002.

XX 18-SEP-2001; 2001JP-00283413.

XX 13-NOV-2000; 2000JP-00345094.

XX (ITOY/) ITO Y.

XX WPI; 2003-508315/48.

XX A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.

XX Example 8; Page 10; 18pp; Japanese.

XX The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
CC leukocyte antigen) peptides of human origin used in an example from the
XX invention

SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 6; Length 9;
Best Local Similarity 88.3%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0;

QY 1 KYHRVIKDF 9
|:|||||
Db 1 KFHVRVIKDF 9

RESULT 8

ADC17701

ID ADC17701 standard; peptide; 9 AA.

XX AC ADC17701;

XX 18-DEC-2003 (first entry)

XX Cyclophilin B protein amino acids 84-92.

XX cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
KW cyclophilin B.

XX Synthetic.

XX WO2003020306-A1.

XX 13-MAR-2003.

XX 28-AUG-2002; 2002WO-JP008641.

XX 29-AUG-2001; 2001JP-00260046.

XX (ITOY/) ITOH K.

XX Itch K, Yamada A;

XX WPI; 2003-300831/29.

XX Desensitizers or allergic reaction suppressors containing peptides
PT originating from the same antigenic substances as reaction-inducing
PT substances, useful for preventing or treating type I allergic diseases
PT and in cancer vaccines.

XX Claim 8; SEQ ID NO 1; 49pp; Japanese.

XX The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet does not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction or
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin E antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 84-92 of the cyclophilin B protein.

XX SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0;

QY 1 KYHRVIKDF 9
|:|||||
Db 1 KFHVRVIKDF 9

RESULT 9

```

ADG89641
ID ADG89641 standard; peptide; 9 AA.
XX
AC ADG89641;
XX
DT 11-MAR-2004 (first entry)
XX
DE Class I HLA-restricted widely expressed antigen #6.
XX
KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS Unidentified.
XX
PN WO2003100027-A2.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-US016736.
XX
PR 28-MAY-2002; 2002US-0383530P.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2004-035134/03.
XX
PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
PS Disclosure; SEQ ID NO 84; 137pp; English.
XX
CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted widely expressed
CC antigen.
XX
SQ Sequence 9 AA;
Query Match 92.0%; Score 46; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHRVIKDF 9
DB 1 KPHRVIKDF 9
RESULT 10
AAY69960
ID AAY69960 standard; peptide; 9 AA.
XX
AC AAY69960;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #40.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label= Phe, Tyr, Met, Trp
FT Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met
XX
ADG89641
ID ADG89641 standard; peptide; 9 AA.
XX
AC ADG89641;
XX
DT 11-MAR-2004 (first entry)
XX
DE Class I HLA-restricted widely expressed antigen #6.
XX
KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; widely antigen.
XX
OS Unidentified.
XX
PN WO2003100027-A2.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-US016736.
XX
PR 28-MAY-2002; 2002US-0383530P.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2004-035134/03.
XX
PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
PS Disclosure; SEQ ID NO 84; 137pp; English.
XX
CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted widely expressed
CC antigen.
XX
SQ Sequence 9 AA;
Query Match 92.0%; Score 46; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHRVIKDF 9
DB 1 KPHRVIKDF 9
RESULT 10
AAY69960
ID AAY69960 standard; peptide; 9 AA.
XX
AC AAY69960;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #40.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /label= Phe, Tyr, Met, Trp
FT Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met
XX
WO967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU ) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX
PI Itoh K, Gomi S;
XX
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
XX
PS Claim 10; Page 59; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 72.0%; Score 36; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KVHRVIKD 8
DB 1 KXHRVIKD 8
RESULT 11
AAR96521
ID AAR96521 standard; peptide; 10 AA.
XX
AC AAR96521;
XX
DT 07-MAR-1997 (first entry)
XX
DE Hepatitis C virus type 9 peptide.
XX
KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;
KW PCR; primer; probe; antibody; infection.
XX
OS Synthetic.
XX
PN WO9613590-A2.
XX
PD 09-MAY-1996.
XX
PF 23-OCT-1995; 95WO-EP004155.
XX
PR 21-OCT-1994; 94EP-00870166.
PR 28-JUN-1995; 95EP-00870076.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Maertens G, Stuyver L;
XX
DR WPI; 1996-251460/25.
XX
PT Hepatitis C virus polynucleic acid unique to unidentified sub.type -
PT used to develop probes and primers for new sub.types and vaccines to
PT prevent and treat infection.
XX
PS Claim 5; Page 68; 150pp; English.
XX
CC The peptides AAR96424-R96524 represent novel peptides derived from the

```

CC novel hepatitis C virus subtypes 1d-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-c or
 CC types 9, 10 or 11 (see AAT2937-T27989). The sequences corresp. to the 5'
 CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.
 CC This sequence is from the HCV subtype 9. The new HCV types were isolated
 CC from patients with chronic HCV from the Benelux countries, France,
 CC Cameroon and Vietnam, because of their aberrant reactivities. The RNA was
 CC extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The
 CC 5'UR, Core/E1 and NS5B regions were sequenced either directly or
 CC partially and used to classify the new viruses into (sub)types based on
 CC comparison with known sequences. The nucleotide sequences can be used to
 CC synthesise probes and primers for the detection of HCV in a sample. The
 CC polypeptides can be used to detect anti-HCV antibodies, for HCV typing or
 CC to prevent HCV infections

XX Sequence 10 AA;

Query Match 62.0%; Score 31; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 31;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYHRVIKD 8

Db |||:|:|

3 KYHQVTQD 10

RESULT 12

AA82292
 ID AAB82292 standard; peptide; 11 AA.

XX AAB82292;

XX 09-JUL-2001 (first entry)

XX Phosphorylation site in potato HMG-CoA reductase.

XX 3-Hydroxy-3-methylglutaryl-CoA reductase; HMG-CoA reductase; HMGR;
 KW phosphorylation; isoprenoid; sterol; transgenic plant; potato;
 KW pathogen resistance; disease resistance; crop protection.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "O-phosphorylated"

XX W0200131043-A1.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-GB004141.

XX 27-OCT-1999; 99GB-00025453.

XX (UYBR-) UNIV BRISTOL.

XX Halford NG, Hey SJ, Beale MH;

XX WPI; 2001-308654/32.

XX Modified 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, useful for
 PT generating transgenic plants having increased isoprenoid production,
 PT comprising a modified phosphorylation site.

XX Claim 16; Page 18; 23pp; English.

XX The present sequence is that of a phosphorylated region of the 3-hydroxy-
 CC 3-methylglutaryl-coenzyme A reductase (HMGR) protein of potato. The
 CC invention relates to modified HMGR genes useful for generating transgenic
 CC plants having increased isoprenoid (especially sterol) production. The
 CC modified genes encode modified HMGR proteins, in which a phosphorylation
 CC site has been rendered inactive by replacing a Ser, Thr or Tyr residue
 CC with Ala or other amino acid residue. This reduces transcriptional
 CC regulation. The HMGR genes may be in the form of mutant plant and

CC plant/non-plant or different plant chimeric genes. Transcriptional
 CC regulation can also be avoided by using heterologous promoters. Increased
 CC seed sterol content has been demonstrated in transgenic plants. The
 CC invention is used to produce plants having increased insect and mite pest
 CC resistance, particularly against species of Homoptera, Diptera,
 CC Lepidoptera, Coleoptera, Hymenoptera, Hemiptera, Dictyoptera, Orthoptera,
 CC arachnids and mites, or it is used to attract beneficial insects,
 CC including Odonata, Hymenoptera, Coleoptera, Neuroptera, or arachnids or
 CC mites to the plant. It is also used to produce plants having increased
 CC pathogen resistance, particularly against a fungus, especially Fusarium,
 CC Aspergillus, Phytophthora, Gaumannomyces, Downy mildews, Colletotrichum,
 CC Cochliobolus, Tapesia, Magnaporthe, Stagnospora, Rhynchosporium,
 CC Septoria, Helminthosporium, and powdery mildews such as Blumeria and
 CC Erysiphe. The modified genes are particularly useful in maize, wheat,
 CC rice, barley, oilseed rape, beans, sunflower, cabbage, potato, spinach,
 CC broccoli, pea, cauliflower, tomato, forest trees, roses and tea. The
 CC invention may also be used to add nutritional benefit such as fat-soluble
 CC vitamins E and K, and sterols to a crop plant

XX Sequence 11 AA;

Query Match 62.0%; Score 31; DB 4; Length 11;

Best Local Similarity 75.0%; Pred. No. 34;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYHRVIKD 8

Db |||:|:|

3 KYNRSIKD 10

RESULT 13

AA69959
 ID AAY69959 standard; peptide; 9 AA.

XX AAY69959;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #39.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX W09967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JF003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOHI) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.

XX Claim 4; Page 61; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumor antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 9 AA;

Query Match

58.0%; Score 29; DB 3; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YHRVVKDF 9
Db :|||||
2 FHRVIEPF 9

RESULT 14
AAAY69924
ID AAY69924 standard; peptide; 11 AA.
XX AC
XX AAY69924;
XX XX
XX 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #4.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX XX
XX PN WO9967288-A1.
XX PD
XX PD 29-DEC-1999.
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.
XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.
XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 50; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

SQ Sequence 11 AA;
Query Match 58.0%; Score 29; DB 3; Length 11;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYHRVI 6
Db :|||||
6 KHRVI 11

RESULT 15
ABG94771
ID ABG94771 standard; peptide; 9 AA.
XX AC
XX ABG94771;
XX XX
XX 02-DEC-2002 (first entry)
XX DE Replicin sequence identified by the 3-point recognition method #44.
XX KW Replicin; glioma; malignin; anthrax; small pox; antiviral; antibacterial;
XX KW 3-point-recognition; vaccine; immunogen; Lethal Factor Protein pX01-107;
XX KW Surface Antigen S Precursor Protein.

OS Polyoma virus.
XX PN US2002120106-A1.
XX XX
XX PD 29-AUG-2002.
XX PF 26-OCT-2001; 2001US-00984056.
XX PR 04-SEP-1998; 98US-00146755.
XX PR 27-MAR-2001; 2001US-00817144.
XX PR 27-MAR-2001; 2001US-0278761P.
XX PR 09-JUL-2001; 2001US-0303396P.
XX XX
XX PA (BOGO/) BOGOCH S.
XX PA (BOGO/) BOGOCH E S.
XX XX
XX PI Bogoch S, Bogoch ES;
XX PI WPI; 2002-691212/74.
XX DR Isolated Bacillus anthracis and small pox virus peptides (I), also known
XX PT as replicins, useful for formulating vaccines for treating anthrax or
XX PT small pox, comprise 7 to 50 amino acids.
XX PS Disclosure; Page 3; 16pp; English.
XX CC The invention relates to isolated Bacillus anthracis and small pox virus
XX CC peptides, also known as replicins, comprising 7 to 50 amino acids
XX CC including at least one lysine residue located six to ten residues from a
XX CC second lysine residue, at least one histidine residue, and at least 6
XX CC lysine residues. The peptides were identified using the 3-point-
XX CC recognition method and based on the replicin sequence isolated from
XX CC glioblastoma cells malignin peptide which is of non-human origin. Also
XX CC included are anti-replicin antibodies (or antibody cocktail), a method of
XX CC stimulating the immune system of a subject to produce antibodies to
XX CC Bacillus anthracis or small pox comprising administering an effective
XX CC amount of at least one or more Bacillus anthracis or small pox replicin
XX CC and an antisense nucleic acid molecule complementary to a mRNA encoding a
XX CC Bacillus anthracis polypeptide (e.g. Anthrax Lethal Factor Protein pX01-
XX CC 107) comprising a replicin sequence, an antisense nucleic acid molecule
XX CC complementary to a mRNA encoding a Small Pox Virus polypeptide (e.g.
XX CC Surface Antigen S Precursor Protein comprising a replicin sequence. The
XX CC peptides are useful for stimulating the immune system of a subject to
XX CC produce antibodies that bind specifically to Anthrax or small pox
XX CC polypeptides containing a replicin sequence. The peptides are useful for
XX CC generating antibodies that can be used in the treatment and/or prevention
XX CC of anthrax or small pox. The peptides are also useful for formulating
XX CC vaccines for treating anthrax or small pox. The present sequence is a
XX CC replicin sequence isolated by the 3-point-recognition system and sharing
XX CC structural similarity with the replicin sequence isolated from
XX CC glioblastoma cells malignin

SQ Sequence 9 AA;
Query Match 56.0%; Score 28; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVVKD 8
Db :|||||
1 KQHRELKD 8

Search completed: October 21, 2004, 07:21:03
Job time : 85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds
(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-39
Sequence: 50
1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	62.0	10	3	US-08-836-075A-204
2	29	58.0	11	4	US-09-418-780A-14
3	29	58.0	11	4	US-09-418-780A-22
4	27	54.0	12	2	US-08-471-286-1
5	25	50.0	11	1	US-08-503-062-8
6	25	50.0	11	5	PCT-US96-11495-8
7	25	50.0	12	2	US-08-973-563A-31
8	25	50.0	12	2	US-08-973-559-31
9	25	50.0	12	3	US-08-993-235-11
10	25	50.0	12	4	US-09-226-666-7
11	25	50.0	12	4	US-08-993-235-11
12	25	50.0	12	4	US-10-037-311B-16
13	24	48.0	11	1	US-08-378-761A-68
14	24	48.0	11	1	US-08-485-286-68
15	23	46.0	12	4	US-09-226-666-17
16	23	46.0	12	5	PCT-US94-05905-10
17	22	44.0	7	2	US-08-292-968-31
18	22	44.0	7	2	US-08-467-974-31
19	22	44.0	7	2	US-08-467-536-31
20	22	44.0	7	3	US-08-467-976-31
21	22	44.0	7	3	US-09-082-514-31
22	22	44.0	8	4	US-09-535-852-1043
23	22	44.0	9	2	US-08-646-981-13
24	22	44.0	9	4	US-09-417-608A-16
25	22	44.0	9	4	US-09-417-608A-41
26	22	44.0	10	2	US-08-556-597-122
27	22	44.0	10	4	US-09-878-281A-264

28	22	44.0	12	1	US-07-778-233B-29	Sequence 29, Appl
29	22	44.0	12	1	US-07-963-321-29	Sequence 29, Appl
30	22	44.0	12	1	US-08-290-641-29	Sequence 29, Appl
31	22	44.0	12	1	US-08-548-540-29	Sequence 29, Appl
32	22	44.0	12	3	US-08-742-243-6	Sequence 6, Appl
33	22	44.0	12	3	US-08-742-243-7	Sequence 7, Appl
34	22	44.0	12	3	US-08-742-243-8	Sequence 8, Appl
35	22	44.0	12	3	US-08-742-243-9	Sequence 9, Appl
36	22	44.0	12	5	PCT-US96-09809-29	Sequence 29, Appl
37	21	42.0	6	4	US-08-877-605-93	Sequence 93, Appl
38	21	42.0	6	4	US-08-877-605-94	Sequence 94, Appl
39	21	42.0	7	2	US-08-188-583-42	Sequence 42, Appl
40	21	42.0	7	2	US-08-292-968-37	Sequence 37, Appl
41	21	42.0	7	2	US-08-623-833B-45	Sequence 45, Appl
42	21	42.0	7	2	US-08-467-974-37	Sequence 37, Appl
43	21	42.0	7	2	US-08-467-536-37	Sequence 37, Appl
44	21	42.0	7	3	US-08-467-976-37	Sequence 37, Appl
45	21	42.0	7	3	US-09-082-514-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-836-075A-204
; Sequence 204, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836.075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-836-075A-204

Query Match 62.0%; Score 31; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
;
; APPLICANT: Kim, Hye-sook
; APPLICANT: Charnecki, Jonathan
; APPLICANT: Putt, David A.
; APPLICANT: Kim, Edward Y.
; TITLE OF INVENTION: PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
; TITLE OF INVENTION: AGAINST CYTOCHROME P450
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Mich-gan
; COUNTRY: US
; ZIP: 48099-4390
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,286
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-301 (Oxford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-286-1

Query Match 54.0%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HRVVKD 8
Db 7 HRVTKD 12

RESULT 5
US-08-503-062-8
; Sequence 8, Application US/08503062
; Patent No. 5723303
; GENERAL INFORMATION:
; APPLICANT: Denis, Gerald V.
; APPLICANT: Green, Michael R.
; TITLE OF INVENTION: NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
; TITLE OF INVENTION: KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/503,062
; FILING DATE: 10-JUL-1995
; CLASSIFICATION: 435

;
; APPLICANT: Kim, Hye-sook
; APPLICANT: Charnecki, Jonathan
; APPLICANT: Putt, David A.
; APPLICANT: Kim, Edward Y.
; TITLE OF INVENTION: PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
; TITLE OF INVENTION: AGAINST CYTOCHROME P450
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Mich-gan
; COUNTRY: US
; ZIP: 48099-4390
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,286
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-301 (Oxford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-286-1

Query Match 58.0%; Score 29; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YHRVIK 7
Db 1 YHKIIK 6

RESULT 3
US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-418-780A-14

Query Match 58.0%; Score 29; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YHRVIK 7
Db 1 YHKIIK 6

RESULT 3
US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-418-780A-22

Query Match 58.0%; Score 29; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YHRVIK 7
Db 1 YHKIIK 6

RESULT 4
US-08-471-286-1
; Sequence 1, Application US/08471286
; Patent No. 5866688
; GENERAL INFORMATION:
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04020/080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-503-062-8

Query Match 50.0%; Score 25; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YHRVIK 7
DB 1 YHDIK 6

RESULT 6
PCT-US96-11495-8
; Sequence 8, Application PC/TUS9611495
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
; TITLE OF INVENTION: NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
; TITLE OF INVENTION: KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11495
; FILING DATE: 03-JUL-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/503,062
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04020/080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-11495-8

Query Match 50.0%; Score 25; DB 5; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YHRVIK 7
DB 1 YHDIK 6

RESULT 7
US-08-973-563A-31
; Sequence 31, Application US/08973563A
; Patent No. 5885965
; GENERAL INFORMATION:
; APPLICANT: Oppenheim, Frank G.
; APPLICANT: Xu, Tao
; APPLICANT: Spacciopoli, Peter
; APPLICANT: Roberts, F. D.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,563A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,273
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-02A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..12
; OTHER INFORMATION: /note="At least one amino acid
; OTHER INFORMATION: must have a D configuration."
US-08-973-563A-31

Query Match 50.0%; Score 25; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYHR 4
DB 6 KYHR 9

RESULT 8
US-08-973-559-31
; Sequence 31, Application US/08973559
; Patent No. 5912230
```

GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: XU TAO
; APPLICANT: ROBERTS, F. D.
; APPLICANT: SPACCIAPOLI, PETER
; APPLICANT: FRIDEN, PHILIP M.
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
; TITLE OF INVENTION: Histatin-Based Peptides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /US/08/973,559
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9340
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-31

Query Match 50.0%; Score 25; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
Db 6 KYHR 9

RESULT 9
US-08-993-235-11
; Sequence 11, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-993-235-11

Query Match 50.0%; Score 25; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
Db 6 KYHR 9

RESULT 10
US-09-226-666-7
; Sequence 7, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
; US-09-226-666-7

Query Match 50.0%; Score 25; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
Db 6 KYHR 9

RESULT 11
US-08-993-235-11
; Sequence 11, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-993-235-11

Query Match 50.0%; Score 25; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KYHR 4
Db 6 KYHR 9

RESULT 12
US-10-037-311B-16

; Sequence 16, Application US/10037311B
; Patent No. 6747190
; GENERAL INFORMATION:
; APPLICANT: MICHIGAN STATE UNIVERSITY
; TITLE OF INVENTION: XYLOGLUCAN FUCOSYLTRANSFERASES
; FILE REFERENCE: MS00-001C2
; CURRENT APPLICATION NUMBER: US/10/037,311B
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US60/117,555
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Cross-species
US-10-037-311B-16

Query Match 50.0%; Score 25; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVVKD 8
|:|:|
DB 6 HQVIRD 11

RESULT 13
US-08-378-761A-68
; Sequence 68, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-68

Query Match 48.0%; Score 24; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVKD 8
|:|:|
DB 3 KKARVVKD 10

RESULT 14

US-08-485-286-68
; Sequence 68, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-68

Query Match 48.0%; Score 24; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVKD 8
|:|:|
DB 3 KKARVVKD 10

RESULT 15

US-09-226-666-17
; Sequence 17, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spaccapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Philip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A

```

; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-17

Query Match      46.0%; Score 23; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 KYHRVIKDF 9
      |:|:|
Db      3 KHKYHKKF 11

```

Search completed: October 21, 2004, 07:29:30
Job time : 22.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVVKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	92.0	9	15	US-10-447-161-84
2	46	92.0	9	16	US-10-788-016-1
3	31	62.0	10	9	US-09-851-138-204
4	29	58.0	11	14	US-10-293-822-14
5	29	58.0	11	14	US-10-293-822-22
6	28	56.0	9	9	US-09-984-056-61
7	28	56.0	9	9	US-09-984-056-62
8	28	56.0	9	9	US-09-984-057-61
9	28	56.0	9	9	US-09-984-057-62
10	28	56.0	9	14	US-10-105-232-61
11	28	56.0	9	14	US-10-105-232-62
12	28	56.0	9	14	US-10-189-437-61
13	28	56.0	9	14	US-10-189-437-62
14	28	56.0	12	15	US-10-601-953-76

15	27	54.0	9	9	US-09-834-765-139	Sequence 139, App
16	27	54.0	9	9	US-09-834-765-419	Sequence 419, App
17	27	54.0	10	9	US-09-834-765-477	Sequence 477, App
18	27	54.0	10	9	US-09-834-765-666	Sequence 666, App
19	25	50.0	10	10	US-09-572-270A-759	Sequence 759, App
20	25	50.0	12	9	US-09-226-666-7	Sequence 7, Appli
21	25	50.0	12	15	US-10-601-953-64	Sequence 64, Appl
22	24	48.0	7	14	US-10-191-540-182	Sequence 182, App
23	24	48.0	9	14	US-10-211-207-23	Sequence 23, Appl
24	24	48.0	9	14	US-10-211-207-24	Sequence 24, Appl
25	24	48.0	9	14	US-10-077-106-23	Sequence 23, Appl
26	24	48.0	9	14	US-10-077-106-24	Sequence 24, Appl
27	23	46.0	8	16	US-10-712-425-1130	Sequence 1130, Ap
28	23	46.0	9	14	US-10-353-929-5	Sequence 5, Appli
29	23	46.0	11	9	US-09-984-056-72	Sequence 72, Appl
30	23	46.0	11	9	US-09-984-057-72	Sequence 72, Appl
31	23	46.0	11	14	US-10-105-232-72	Sequence 72, Appl
32	23	46.0	11	14	US-10-189-437-72	Sequence 72, Appl
33	23	46.0	12	9	US-09-226-666-17	Sequence 17, Appl
34	22	44.0	7	14	US-10-105-232-265	Sequence 265, App
35	22	44.0	7	14	US-10-405-339-26	Sequence 26, Appl
36	22	44.0	7	14	US-10-405-339-39	Sequence 39, Appl
37	22	44.0	7	14	US-10-405-339-42	Sequence 42, Appl
38	22	44.0	7	14	US-10-189-437-252	Sequence 252, App
39	22	44.0	9	16	US-10-730-454-16	Sequence 16, Appl
40	22	44.0	9	16	US-10-730-454-41	Sequence 41, Appl
41	22	44.0	10	9	US-09-819-308-29	Sequence 29, Appl
42	22	44.0	10	10	US-09-899-046-264	Sequence 264, App
43	22	44.0	10	10	US-09-878-281-264	Sequence 264, App
44	22	44.0	10	10	US-09-873-224-264	Sequence 264, App
45	22	44.0	11	9	US-09-795-006A-128	Sequence 128, App

ALIGNMENTS

RESULT 1
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 92.0%; Score 46; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYHRVVKDF 9
Db 1 KYHRVVKDF 9

RESULT 2
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US2004014192A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyoto

```
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophilin B
US-10-788-016-1

Query Match          92.0%; Score 46; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KYHRVIKDF 9
       |:|||||
Db      1 KHRVIKDF 9

RESULT 3
US-09-851-138-204
; Sequence 204, Application US/09851138
; Publication No. US2002018508A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/851,138
; FILING DATE: 09-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,075
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204
```

```
Query Match          62.0%; Score 31; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 KYHRVIKND 8
       |:|:|:|
Db      3 KYHQVTQD 10

RESULT 4
US-10-293-822-14
; Sequence 14, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-822-14
```

```
Query Match          58.0%; Score 29; DB 14; Length 11;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 YHRVIK 7
       |:|:|
Db      1 YHKLIK 6

RESULT 5
US-10-293-822-22
; Sequence 22, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-293-822-22
```

```
Query Match          58.0%; Score 29; DB 14; Length 11;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 YHRVIK 7
       |:|:|
```

Db 1 YHKIUK 6

RESULT 6

US-09-984-056-61
; Sequence 61, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-61

Query Match 56.0%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVVKD 8
| | | : | |
Db 1 KQRELKD 8

RESULT 7

US-09-984-056-62
; Sequence 62, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-056-62

Query Match 56.0%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVVKD 8
| | | : | |
Db 1 KQRELKD 8

RESULT 8

US-09-984-057-61
; Sequence 61, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-09-984-057-61

Query Match 56.0%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVVKD 8
| | | : | |
Db 1 KQRELKD 8

RESULT 9

US-09-984-057-62
; Sequence 62, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus

US-09-984-057-62

Query Match 56.0%; Score 28; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVTKD 8
| | | : | |
Db 1 KQHRELKD 8

RESULT 10

US-10-105-232-61
; Sequence 61, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Patentin 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-61

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVTKD 8
| | | : | |
Db 1 KQHRELKD 8

RESULT 11

US-10-105-232-62
; Sequence 62, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535

; SOFTWARE: Patentin 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-105-232-62

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVTKD 8
| | | : | |
Db 1 KQHRELKD 8

RESULT 12

US-10-189-437-61
; Sequence 61, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: Patentin 2.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-61

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVTKD 8
| | | : | |
Db 1 KQHRELKD 8

RESULT 13

US-10-189-437-62
; Sequence 62, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: Patentin 2.1

; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-62

Query Match 56.0%; Score 28; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KYHRVIKD 8
| : : :
Db 1 KQHRELKD 8

RESULT 14
US-10-601-953-76
; Sequence 76, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-76

Query Match 56.0%; Score 28; DB 15; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HRVIKDF 9
| : : :
Db 1 HNIQDF 7

RESULT 15
US-09-834-765-139
; Sequence 139, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-139

Query Match 54.0%; Score 27; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YHRVIKDF 9
| : : :
Db 1 YEHVIKNF 8

Search completed: October 21, 2004, 07:33:43
Job time : 62.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	40.0	10	2 S36849	Ig heavy chain V r
2	19	38.0	12	2 PC4377	telomeric and tetr
3	18	36.0	11	2 I54193	Rhesus blood group
4	17	34.0	10	2 PC4374	telomeric and tetr
5	17	34.0	10	2 JQ0943	hypothetical 1.3K
6	16	32.0	8	2 S65381	cytochrome-c oxida
7	16	32.0	10	2 B39308	glycine reductase
8	16	32.0	11	2 S23373	T-cell receptor al
9	16	32.0	12	2 G64003	hypothetical prote
10	15	30.0	7	1 NYPG7	hypothetical hepta
11	15	30.0	10	2 S13224	virG protein - Agr
12	15	30.0	10	2 AS9272	peptide-N4-(N-acet
13	15	30.0	11	2 PC2330	cycloinulooligosc
14	15	30.0	11	4 I52708	ELAV-like neuronal
15	15	30.0	12	2 S10624	lipovitellin - Afr
16	15	30.0	12	2 PT0228	Ig heavy chain CDR
17	15	30.0	12	2 PQ0730	unidentified 5.4/3
18	14	28.0	6	2 B44510	hypothetical prote
19	14	28.0	7	2 PT0246	Ig heavy chain CRD
20	14	28.0	8	2 S66296	Na+-transporting A
21	14	28.0	9	2 C36730	hutu protein - Kle
22	14	28.0	9	2 S78420	ribosomal protein
23	14	28.0	9	2 A44787	calliFMRFamide 10
24	14	28.0	9	2 I49406	bone gla protein -
25	14	28.0	10	2 B56899	serum heterodimer,
26	14	28.0	11	2 G42762	proteasome endopep
27	14	28.0	11	2 PQ0733	unidentified 6.0/1
28	14	28.0	11	2 PH1376	T antigen variant
29	14	28.0	11	2 PN0042	stathmin - mouse (

30	14	28.0	12	2 S09082	proteasome chain 1
31	14	28.0	12	2 S34447	binR protein - Sta
32	13	26.0	6	2 S02617	alcohol dehydrogen
33	13	26.0	6	2 B56979	collagen alpha 1(I
34	13	26.0	8	2 S69165	ferredoxin a2 - Ja
35	13	26.0	9	2 T31612	hypothetical prote
36	13	26.0	9	2 PT0315	Ig heavy chain CRD
37	13	26.0	9	2 A42266	peptidylglycine mo
38	13	26.0	9	2 D57444	neurotrophin Grb-A
39	13	26.0	9	2 A41978	calliFMRFamide 1 -
40	13	26.0	9	2 B41978	calliFMRFamide 2 -
41	13	26.0	9	2 C41978	calliFMRFamide 3 -
42	13	26.0	9	2 D41978	calliFMRFamide 4 -
43	13	26.0	9	2 B41978	calliFMRFamide 5 -
44	13	26.0	9	2 F41978	calliFMRFamide 6 -
45	13	26.0	9	2 G41978	calliFMRFamide 7 -

ALIGNMENTS

RESULT 1

S36849
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36849
R/Jacob, J.; Kelsoc, G.
Submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)
A:Reference number: S25024
A:Accession: S36849
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-10 <JAC>
A:Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:e51590; PID:gl333861
C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 20; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KYHRVIKDF 9
:|:|:|:
Db 2 RYRTVVVNF 10

RESULT 2

PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C:Accession: PC4377
R/Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI
A:Reference number: PC4371; MUID:97445086; PMID:9299414
A:Accession: PC4377
A:Molecule type: protein
A:Residues: 1-12 <SAR>
A:Cross-references: UNIPROT:Q9QX80; UNIPROT:Q9Z0U8; UNIPROT:O88311; UNIPROT:Q9QX81
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 38.0%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KYHRV 5
:|:|:
Db 3 KFTTV 7

RESULT 3

I54193
Rhesus blood group CcEe protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I54193
R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Coliin, Y.
Genomics 19, 68-74, 1994
A>Title: Organization of the gene (RHCE) encoding the human blood group RBCcEe antigens
A:Reference number: I54193; MUID:94245182; PMID:8188244
A:Accession: I54193
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: UNIPROT:Q9UPC8; UNIPROT:Q99906; UNIPROT:Q9UK19; UNIPROT:Q9UPN0; UNIPROT:Q9UEC7; GB:S70456; NID:G546795; PIDN:AAD14061.1; PID:G4261761
C:Genetics:
A:Gene: GDB:RHCE
A:Cross-references: GDB:229957; OMIM:111700
A:Map position: lp36.2-1p34

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KYHRVIX 7
|||
DB 4 KYPRSVR 10

RESULT 4
PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4374
R;Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A>Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A:Reference number: PC4371; MUID:97445086; PMID:9299414
A:Accession: PC4374
A:Molecule type: protein
A:Residues: 1-10 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KYHRV 5
|||
DB 6 KEHRL 10

RESULT 5
JQ0943
hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)
C:Species: Infectious bursal disease virus
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JQ0943
R;Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bours
J. Gen. Virol. 71, 1303-1312, 1990
A>Title: A comparison of the sequences of segment A of four infectious bursal disease vi
A:Reference number: JQ0941; MUID:90278420; PMID:2161302
A:Accession: JQ0943
A>Status: translation not shown
A:Molecule type: genomic RNA
A:Residues: 1-10 <RAY>
A:Cross-references: UNIPROT:Q82625; GB:D00869; NID:G221038; PIDN:BAA00743.1; PID:dl00120

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYH 3
:|||
DB 8 RYH 10

RESULT 6
S65381
cytochrome-c oxidase (EC 1.9.3.1) chain V1b, hepatic - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65381
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A>Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termi
A:Reference number: S65372; MUID:95324529; PMID:7601105
A:Accession: S65381
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <SCH>
A:Cross-references: UNIPROT:P80430
C:Keywords: oxidoreductase

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHR 4
:|||
DB 6 FHR 8

RESULT 7
B39308
glycine reductase (EC 1.4.99.-) sulfhydryl protein C, beta chain - Clostridium sticklandii
C:Species: Clostridium sticklandii
C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 09-Jul-2004
C:Accession: B39308
R;Stadtman, T.C.; Davis, J.N.
J. Biol. Chem. 266, 22147-22153, 1991
A>Title: Glycine reductase protein C. Properties and characterization of its role in the
A:Reference number: A39308; MUID:92042141; PMID:1939235
A:Accession: B39308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <STA>
A:Cross-references: UNIPROT:Q9EV92
C:Function:
A:Description: glycine reductase complex catalyzes the reductive deamination of glycine t
C:Keywords: ATP; oxidoreductase

Query Match 32.0%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIK 8
:|||
DB 4 NKVIAD 9

RESULT 8
S23373
T-cell receptor alpha chain J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23373
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmann
Eur. J. Immunol. 21, 2749-2754, 1991
A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu
A:Reference number: S23364; MUID:92037820; PMID:1657615
A:Accession: S23373
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-11 <PLU>

A;Cross-references: EMBL:X59168
C;Keywords: T-cell receptor

Query Match 32.0%; Score 16; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YHRVI 6
| : ||
Db 6 YDKVI 10

RESULT 9

G64003
hypothetical protein HI0195 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
C;Accession: G64003
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.F.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Smali, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64003
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <TIGR>
A;Cross-references: GB:U32704; GB:L42023; NID:G1573143; PID:G1573155; TIGR:HI0195

Query Match 32.0%; Score 16; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.4e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVH 3
| : ||
Db 4 QYH 6

RESULT 10

NYPG7
hypothalamic heptapeptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release
A;Reference number: A01417; MUID:81213980; PMID:6263778
A;Accession: A01417
A;Molecule type: protein
A;Residues: 1-7 <CHA>
A;Cross-references: UNIPROT:P01153
C;Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus

Query Match 30.0%; Score 15; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YH 3
| : ||
Db 3 YH 4

RESULT 11

SI3224
virG protein - Agrobacterium sp. (fragment)
C;Species: Agrobacterium sp.
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: SI3224
R;Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.

J. Mol. Biol. 215, 537-547, 1990
A;Title: Binding of the regulatory protein VirG to the phased signal sequences upstream of
A;Reference number: SI3224; MUID:91093316; PMID:2231718
A;Accession: SI3224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAM>
A;Cross-references: UNIPROT:Q7MOP7

Query Match 30.0%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYHRVIMKD 8
| : ||
Db 2 KHVIVIDD 9

RESULT 12

A59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chain -
A;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K. Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: A59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
A;Cross-references: UNIPROT:P81899
C;Keywords: hydrolase

Query Match 30.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YH 3
| : ||
Db 5 YH 6

RESULT 13

PC2330
cyclooligosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-2554)
C;Species: Bacillus circulans
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: PC2330
R;Kushibe, S.; Mitsui, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y. Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A;Title: Purification and characterization of cyclooligosaccharide fructanotransferase
A;Reference number: PC2330; MUID:95201377; PMID:7765973
A;Accession: PC2330
A;Molecule type: protein
A;Residues: 1-11 <KUS>
A;Cross-references: UNIPROT:Q7MOL3
C;Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 30.0%; Score 15; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YH 3
| : ||
Db 1 YH 2

RESULT 14

IS2708

ELAV-like neuronal protein 1, truncated splice form - human
 N:Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
 C:Species: Homo sapiens (man)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C:Accession: I52708
 R:Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
 Cancer Res. 54, 4988-4992, 1994
 A>Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis
 A:Reference number: I52708; MUID:94349312; PMID:8069866
 A:Accession: I52708
 A>Status: translated from GE/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-11 <SEK>
 A:Cross-references: UNIPROT:Q16234; GB:S73887; NID:q688242; PIDN:AMD14142.1; PID:q426184
 C:Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
 C:Genetics:
 A:Gene: GDB:ELAVL4; HUD; PNEM
 A:Cross-references: GDB:I41875; OMIM:168360
 A:Map position: lp36-lp36
 C:Keywords: alternative splicing

Query Match 30.0%; Score 15; DB 4; Length 11;
 Best Local Similarity 50.0%; Pred. No. 9.1e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVIK 7
 |::|
 Db 6 RIUK 9

RESULT 15
 S10624
 lipovitellin - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S10624
 R:Wallace, R.A.; Hoch, K.L.; Carnevali, O.
 J. Mol. Biol. 213, 407-409, 1990
 A>Title: Placement of small lipovitellin subunits within the vitellogenin precursor in X
 A:Reference number: S10624; MUID:90278951; PMID:2352275
 A:Accession: S10624
 A:Molecule type: protein
 A:Residues: 1-12 <WAL>

Query Match 30.0%; Score 15; DB 2; Length 12;
 Best Local Similarity 42.9%; Pred. No. 1e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KYHRVIK 7
 |::|
 Db 1 KFORPYK 7

Search completed: October 21, 2004, 07:27:59
 Job time : 16.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-39
Perfect score: 50
Sequence: 1 KYHRVVKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	44.0	9	Q7SCD2	neurospora
2	21	42.0	8	Q8AWV7	anas platyr
3	21	42.0	8	Q8AWV8	cygnus colu
4	21	42.0	8	Q8AWV9	anser caeru
5	21	42.0	8	Q8AWW0	coscoroba c
6	21	42.0	11	Q9XSP2	hyllobates s
7	21	42.0	11	Q9XSP5	pan troglod
8	21	42.0	11	Q9XSP6	pongo pygma
9	21	42.0	11	Q9XSP7	pygathrix n
10	21	42.0	11	Q9XSP8	presbytis j
11	21	42.0	11	Q9XSP4	gorilla gor
12	20	40.0	8	Q05403	saccharomyc
13	20	40.0	10	Q9TQV4	e equus cab
14	20	40.0	12	Q9TT29	saguinus oe
15	20	40.0	12	Q9TT31	callithrix
16	19	38.0	10	Q8N6B1	homo sapien
17	18	36.0	12	Q7RGG4	plasmodium
18	17	34.0	9	B343_SERPL	seriatia pl
19	17	34.0	9	Q9TWX7	manduca sex
20	17	34.0	9	Q8MJN1	cebuella py
21	17	34.0	9	Q8MJN2	callithrix
22	17	34.0	9	Q8MJN3	callimico g
23	17	34.0	9	Q8MJN4	leontopithe
24	17	34.0	9	Q8MJN5	saguinus fu
25	17	34.0	9	Q8MJN6	aotus azara
26	17	34.0	9	Q8MJN7	saimiri sci
27	17	34.0	9	Q8MJN8	cebus apell
28	17	34.0	9	Q8MJN9	ateles fusc
29	17	34.0	10	Q93LX4	vibrio chol
30	17	34.0	10	Q8RJF1	pseudomonas
31	17	34.0	10	Q82625	avian infec

Q8mel7 sida hooker
Q8mel9 pavonia has
Q8mem2 lagunaria p
Q8nep0 hibiscus pe
Q8nep3 hibiscus no
Q8nep5 hibiscus wi
Q8nep7 hibiscus dr
Q8mer0 hibiscus co
Q8mer1 hibiscus ca
Q8mer7 floria viti
Q8mer8 dombeya til
Q8mes1 alyogyne pi
Q8mes3 alyogyne cr
Q8mes5 abelmoschus

ALIGNMENTS

RESULT 1
Q7SCD2 PRELIMINARY; PRT; 9 AA.
ID Q7SCD2;
AC Q7SCD2;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU05334.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]_TaxID=5141;
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Selitrennikoff C.P., Pedersen D., Nelson M., Washburne M.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanvaselis M., Mauceli E., Biele C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Yarden O., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000130; EAA34319.1; -;
SQ SEQUENCE 9 AA; 1173 MW; C483A32B50440449 CRC64;

Query Match 44.0%; Score 22; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.8e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YHRVVKD 8
: : : : :
Db 2 FNRIYKD 8

RESULT 2
Q8AWV7 PRELIMINARY; PRT; 8 AA.
ID Q8AWV7
AC Q8AWV7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

```

DE LDH-B (Fragment).
GN Name-LDH-B;
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]_
RP SEQUENCE FROM N.A.
RA Catter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123327; AAM96901.1; -.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match
Best Local Similarity 42.0%; Score 21; DB 2; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
Db 2 HKIVAD 7

RESULT 3
Q8AWV8 PRELIMINARY; PRT; 8 AA.
AC Q8AWV8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name-LDH-B;
OS Cygnus columbianus (tundra swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.
OX NCBI_TaxID=110926;
RN [1]_
RP SEQUENCE FROM N.A.
RA Catter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123326; AAM96900.1; -.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match
Best Local Similarity 42.0%; Score 21; DB 2; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
Db 2 HKIVAD 7

RESULT 4
Q8AWV9 PRELIMINARY; PRT; 8 AA.
AC Q8AWV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name-LDH-B;
OS Anser caerulescens (snow goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=70340;
RN [1]_
RP SEQUENCE FROM N.A.
RA Catter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123325; AAM96899.1; -.

DE LDH-B (Fragment).
GN Name-LDH-B;
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]_
RP SEQUENCE FROM N.A.
RA Catter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123327; AAM96901.1; -.

FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match
Best Local Similarity 42.0%; Score 21; DB 2; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
Db 2 HKIVAD 7

RESULT 5
Q8AWW0 PRELIMINARY; PRT; 8 AA.
AC Q8AWW0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE LDH-B (Fragment).
GN Name-LDH-B;
OS Coscoroba coscoroba (Coscoroba swan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
OX NCBI_TaxID=8863;
RN [1]_
RP SEQUENCE FROM N.A.
RA Catter J.-P., StJohn J., Quinn T.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY123324; AAM96898.1; -.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 911 MW; D73AAD2C05331F1 CRC64;

Query Match
Best Local Similarity 42.0%; Score 21; DB 2; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
Db 2 HKIVAD 7

RESULT 6
Q8XSP2 PRELIMINARY; PRT; 11 AA.
AC Q8XSP2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]_
RP SEQUENCE FROM N.A.
RA MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243280; CAB45927.1; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match
Best Local Similarity 50.0%; Score 21; DB 2; Length 11;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YHRV1K 7
```

```

Db          6 HRSVK 11

RESULT 7
Q9XSP5      PRELIMINARY;      PRT;      11 AA.
AC
Q9XSP5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243277; CAB45926.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

RESULT 8
Q9XSP6      PRELIMINARY;      PRT;      11 AA.
AC
Q9XSP6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243279; CAB45925.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

RESULT 9
Q9XSP7      PRELIMINARY;      PRT;      11 AA.
AC
Q9XSP7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243282; CAB45924.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

```

```

AC
Q9XSP7;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243282; CAB45924.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

RESULT 10
Q9XSP8      PRELIMINARY;      PRT;      11 AA.
AC
Q9XSP8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Presbytis johnii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Presbytis.
OX NCBI_TaxID=98375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243281; CAB46033.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

RESULT 11
Q9XSP9      PRELIMINARY;      PRT;      11 AA.
AC
Q9XSP9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN Name=PDGFA;
OS Presbytis johnii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Presbytis.
OX NCBI_TaxID=98375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243281; CAB46033.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          2 YHRVVK 7
Db          6 HRSVK 11

```

```
GN Name=PDGFA;
OS Gorilla gorilla (gorilla);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243278; CAB45916.1; -.
FT NON_TER 1
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 42.0%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YHRVIX 7
Db :|||
6 HHRVIX 11

RESULT 12
Q05403
ID Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Orf 00915 protein (Fragment).
GN Name=orf 00915;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29,425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIX 7
Db :|||
3 HNVVX 7

RESULT 13
Q9TQV4
ID Q9TQV4 PRELIMINARY; PRT; 10 AA.
AC Q9TQV4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Equus caballus pop-variant * transferrin (Equus caballus clone 7 transferrin) (Equus caballus pop-variant F1 transferrin) (Equus caballus pop-variant F2 transferrin) (Equus caballus pop-variant D transferrin) (Equus caballus pop-variant H2 transferrin) (Equus caballus pop-variant O transferrin) (Equus caballus pop-variant F3 transferrin) (Equus caballus pop-variant G transferrin) (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243278; CAB45916.1; -.
FT NON_TER 1
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHRV 5
Db :|||
7 FHRV 10

RESULT 14
Q9TT29
ID Q9TT29 PRELIMINARY; PRT; 12 AA.
AC Q9TT29;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20188801; PubMed=10723742;
RA Francino M.P., Ochman H.;
RT "Strand symmetry around the beta-globin origin of replication in primates.";
RL Mol. Biol. Evol. 17:416-422(2000).
DR EMBL; AF205415; AAF23766.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1251 MW; 07BC8AFAB8D72DD4 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYH 3
Db :|||
10 KYH 12

RESULT 15
Q9TT31
ID Q9TT31 PRELIMINARY; PRT; 12 AA.
AC Q9TT31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
```

OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=20188801; PubMed=10723742;
 RA Francino M.P., Ochman H.;
 RT "Strand symmetry around the beta-globin origin of replication in
 RL Mol. Biol. Evol. 17:416-422(2000).
 DR EMBL; AF205413; AAF23764.1; -.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1251 MW; 07BC8APAE8D72DD4 CRC64;

Query Match 40.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KYH 3
 |||
 Db 10 KYH 12

Search completed: October 21, 2004, 07:26:50
 Job time : 87 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:04:19 ; Search time 83 Seconds
(without alignments)
38.898 Million cell updates/sec

Title: US-09-720-469A-40

Perfect score: 51

Sequence: 1 DYMIQGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 23Sep04: *
1: genesep1980s: *
2: genesep1990s: *
3: genesep2000s: *
4: genesep2001s: *
5: genesep2002s: *
6: genesep2003as: *
7: genesep2003bs: *
8: genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3	Aay69963 Human cyc
2	51	100.0	9	4	Aab46947 Human cyc
3	51	100.0	9	3	Adci17709 Modified
4	47	92.2	9	3	Aay69922 Human cyc
5	47	92.2	9	4	Aab46931 Human cyc
6	47	92.2	9	4	Aag68089 Antitumou
7	47	92.2	9	5	Abg79076 Human Cyc
8	47	92.2	9	6	Ab84374 Human Cyc
9	47	92.2	9	7	Adci17702 Cyclophil
10	47	92.2	9	8	Adg89642 Class I H
11	41	80.4	9	3	Aay69958 Human cyc
12	37	72.5	9	3	Aay69961 Human cyc
13	36	70.6	9	3	Aay69957 Human cyc
14	27.5	53.9	12	2	Aap91898 KGF-b min
15	27	52.9	9	2	Aar45361 Choline o
16	27	52.9	9	6	Abri16438 Human can
17	27	52.9	9	6	Abri16847 Human can
18	27	52.9	9	6	Abri16768 Human can
19	27	52.9	9	6	Abri16188 Human can
20	27	52.9	9	6	Abri16609 Human can
21	27	52.9	10	6	Abri17313 Human can
22	27	52.9	10	6	Abri16875 Human can
23	27	52.9	10	6	Abri16266 Human can
24	27	52.9	10	6	Abri16954 Human can
25	27	52.9	10	6	Abri16696 Human can

26	27	52.9	10	6	ABR16761	Human can
27	27	52.9	10	6	ABR16123	Human can
28	27	52.9	10	6	ABR16487	Human can
29	27	52.9	10	6	ABR17152	Human can
30	27	52.9	10	6	ABR16466	Human can
31	27	52.9	10	6	ABR16141	Human can
32	27	52.9	10	6	ABR16299	Human can
33	27	52.9	10	6	ABR16898	Human can
34	26	51.0	9	2	AAR72938	E. coli P
35	26	51.0	9	2	AAR72894	E. coli P
36	26	51.0	9	8	ADP49294	Natriuret
37	26	51.0	9	8	ADP49297	Natriuret
38	26	51.0	10	2	AAR72949	E. coli P
39	26	51.0	10	2	AAR72905	E. coli P
40	26	51.0	10	4	AAW42948	Mycoplasma
41	26	51.0	12	2	AAW21441	HSV glyco
42	26	51.0	12	6	AAO31067	Human P8
43	25	49.0	9	2	AAR20729	Pancreas-
44	25	49.0	9	3	AAV51905	Elastase
45	25	49.0	9	4	AAW22987	HIV pepti

ALIGNMENTS

RESULT 1
AAY69963
ID AAY69963 standard; peptide; 9 AA.

XX AC AAY69963;
XX 11-APR-2000 (first entry)
XX Human cyclophilin B peptide fragment #43.
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

PN WO9967288-A1.

XX 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.
(ITOH/) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

PT Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.

XX Claim 10; Page 60; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 3; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQGDF 9

|||||

```

Db          1 DYMIOGGDF 9

RESULT 2
AAB46947
ID AAB46947 standard; peptide; 9 AA.
XX
XX AC AAB46947;
XX
XX
XX 04-MAY-2001 (first entry)
XX
XX Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.
XX
XX Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
XX virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
XX viral infectious disease; cyclophilin B; human.
XX
XX Homo sapiens.
XX
XX EP1074267-A1.
XX
XX 07-FEB-2001.
XX
XX 24-JUL-2000; 2000EP-00306263.
XX
XX 22-JUL-1999; 99JP-00207687.
XX
XX (SUMU ) SUMITOMO PHARM CO LTD.
XX
XX Takasu H, Gotch M, Yamaoka T;
XX WPI; 2001-193144/20.
XX
XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
XX the manufacture of an agent for the induction of antigen-specific T
XX cells.
XX
XX Disclosure; Page 20; 25pp; English.
XX
XX This invention describes the novel use of interferons (IFNs) or DNAs
XX capable of expressing the interferons and/or antigenic proteins (AP) ,
XX antigenic peptides derived from the proteins or DNAs capable of
XX expressing the antigenic proteins or peptides, in the manufacture of an
XX agent for induction of antigen-specific T cells. The products of the
XX invention have virucide and cytostatic activity and can be used for gene
XX therapy or as inducers of antigen-specific T cells. The action of
XX interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
XX T cell (CTL) by administering an antigenic peptide in an incomplete
XX Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
XX DNA encoding IFNs) are useful in the manufacture of a medicament for
XX inducing antigen-specific T cells in an individual who has been
XX administered with AP (or DNA encoding AP) or vice versa. The medicament
XX is useful for the treatment or prophylaxis of a tumor or a viral
XX infectious disease
XX
XX Sequence 9 AA;

Query Match          100.0%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 DYMIOGGDF 9
           |||||
Db          1 DYMIOGGDF 9

RESULT 4
AAY69922
ID AAY69922 standard; peptide; 9 AA.
XX
XX AC AAY69922;
XX
XX 11-APR-2000 (first entry)
XX
XX Human cyclophilin B peptide fragment #2.
XX
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
XX
XX WO9967288-A1.
XX
XX 29-DEC-1999.

```

Modified cyclophilin B protein amino acids 91-99.

cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen; allergy; epitope; cancer; immunoglobulin E antibody; desensitization; cyclophilin B.

Synthetic.

WO2003020306-A1.

13-MAR-2003.

28-AUG-2002; 2002WO-JPO08641.

29-AUG-2001; 2001JP-00260046.

(ITOH/) ITOH K.

Itch K, Yamada A;

WPI; 2003-300811/29.

Desensitizers or allergic reaction suppressors containing peptides originating from the same antigenic substances as reaction-inducing substances, useful for preventing or treating type I allergic diseases and in cancer vaccines.

Claim 8; SEQ ID NO 9; 49pp; Japanese.

The invention relates to allergic reaction suppressors, comprising a peptide which originates from the same antigenic substance as the antigenic substance inducing the (peptide-originated) allergic reaction, and containing an epitope different from the epitope participating in the induction of the allergic reaction and yet does not induce the allergic reaction. The desensitizers or allergic reaction suppressors are useful for treating and preventing type I allergic diseases and in cancer vaccines for preventing or treating cancer. The allergic reaction or suppressors are also useful for suppressing an allergic reaction or reducing immunoglobulin E antibody production, and for desensitization to antigens. This sequence represents a peptide used in the invention and corresponds to amino acids 91-99 of the cyclophilin B protein with the Phe at position 92 replaced by a Tyr.

Sequence 9 AA;

Query Match 100.0%; Score 51; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIOGGDF 9
 |||||
Db 1 DYMIOGGDF 9

RESULT 4

AAY69922

ID AAY69922 standard; peptide; 9 AA.

XX AC AAY69922;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #2.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.
 XX 25-JUN-1998; 98JP-00178449.
 XX (SUMU) SUMITOMO PHARM CO LTD.
 XX (ITOH/) ITOH K.
 XX Itoh K, Gomi S;
 XX WPI; 2000-116932/10.
 XX Tumor antigen peptides derived from cyclophilin B for treatment and
 XX diagnosis of tumors.
 XX Claim 4; Page 49; 64pp; Japanese.
 XX This sequence represents a cyclophilin B peptide of the invention. The
 XX peptides are tumour antigen peptides derived from cyclophilin B, that
 XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 XX peptides are used for the treatment and diagnosis of tumours
 XX Sequence 9 AA;
 XX
 XX Query Match 92.2%; Score 47; DB 3; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYMIQGGDF 9
 DB 1 DFMIQGGDF 9
 RESULT 5
 AAB46931
 ID AAB46931 standard; peptide; 9 AA.
 AC AAB46931;
 DT 04-MAY-2001 (first entry)
 DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
 KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
 KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 KW viral infectious disease; cyclophilin B; human.
 OS Homo sapiens.
 PN EP1074267-A1.
 XX 07-FEB-2001.
 XX 24-JUL-2000; 2000EP-00306263.
 XX 22-JUL-1999; 99JP-00207687.
 XX (SUMU) SUMITOMO PHARM CO LTD.
 XX Takasu H, Gotch M, Yamaoka T;
 XX WPI; 2001-193144/20.
 XX Use of antigenic proteins, peptides, interferon or their encoding DNA, in
 XX the manufacture of an agent for the induction of antigen-specific T
 XX cells.
 XX Disclosure; Page 15; 25pp; English.
 XX This invention describes the novel use of interferons (IFNs) or DNAs
 XX capable of expressing the interferons and/or antigenic proteins (AP),
 XX antigenic peptides derived from the proteins or DNAs capable of
 XX expressing the antigenic proteins or peptides, in the manufacture of an

CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease
 XX Sequence 9 AA;
 XX
 XX Query Match 92.2%; Score 47; DB 4; Length 9;
 XX Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 XX Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYMIQGGDF 9
 DB 1 DFMIQGGDF 9
 RESULT 6
 AAG68089
 ID AAG68089 standard; peptide; 9 AA.
 XX AAG68089;
 AC AAG68089;
 DT 17-DEC-2001 (first entry)
 DE Antitumour peptide cyclophilin B 91-99.
 KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;
 KW cyclophilin B gene; HLA-A2402.
 OS Homo sapiens.
 PN JP2001245675-A.
 XX 11-SEP-2001.
 XX 25-DEC-2000; 2000JP-00393047.
 XX 28-DEC-1999; 99JP-00374322.
 XX (ITOY/) ITO Y.
 XX WPI; 2001-610076/70.
 XX New peptides for recognizing cancer cells with tumor specific cytotoxic T
 XX lymphocytes and for treating cancer.
 XX Claim 8; Page 2; 14pp; Japanese.
 XX The present invention describes peptides recognising cancer cells with
 XX tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising
 XX cancer cells with tumour specific CTLs are selected from: (1) peptides of
 XX sequences (AAG68066 to AAG68069); (2) peptides containing the above
 XX mentioned sequences; (3) peptides having 70 % or more of homogeneity with
 XX the above mentioned sequences; and (4) peptides with one or more deleted,
 XX substituted, added or inserted amino acid(s) of the above mentioned
 XX sequences, particularly those having recognising property due to HLA-
 XX A2402 binding CTL, especially having at least 5 amino acids, used for
 XX medicine, particularly anticancer agents, derived from antitumour
 XX antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B
 XX genes. The antitumour peptides have cytostatic activities. The peptides
 XX are used for the treatment of cancer. The peptides cause activation of
 XX CTL in cancer patients. The present sequence represents a peptide from
 XX the present invention
 XX Sequence 9 AA;
 XX

Query Match 92.2%; Score 47; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQGGDF 9
|:|||||
Db 1 DFMIQGGDF 9

RESULT 7
ABG79076
ID ABG79076 standard; peptide; 9 AA.
XX
AC ABG79076;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human Cyp-B class I HLA widely expressed antigen peptide #2.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.

The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigen-associated CPP to (I), where antigen enters into the cell. The antigens are, for example, tumour antigen derived epitopes recognised by tumour infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention

XX
SQ Sequence 9 AA;
Query Match 92.2%; Score 47; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQGGDF 9
|:|||||
Db 1 DFMIQGGDF 9

RESULT 8
ABR84374
ID ABR84374 standard; peptide; 9 AA.
XX
AC ABR84374;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human CypB HLA-A24 epitope, SEQ ID NO:24.
XX
KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A24 epitope.
XX
OS Homo sapiens.
XX
PN JP2002365286-A.
XX
PD 18-DEC-2002.
XX
PF 18-SEP-2001; 2001JP-00283413.
XX
PR 13-NOV-2000; 2000JP-00345094.
XX
PA (ITOV/) ITO Y.
XX
DR WPI; 2003-508315/48.
XX
PT A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.
XX
PS Example 8; Page 10; 18pp; Japanese.

The invention relates to a method for the detection of antigen specific T-cells in a blood sample involving the use of a plurality of antigenic peptides. The method comprises sampling of peripheral blood monocytes; stimulation of the collected peripheral blood monocytes with antigens without direct use of antigen presenting cells; and detection of T-cells specific to the antigen in the stimulated monocytes. The method is particularly used for the detection of cancer as it can be used in semi-quantitative determination of cancer specific T-cells. It can also be used for cancer vaccine therapy for patients with cervical or prostate cancer. The method can additionally be used to monitor of cellular immunity and cancer immune therapy by detection of specific T-cell frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human leukocyte antigen) peptides of human origin used in an example from the invention

QY 1 DYMIQGGDF 9
|:|||||
Db 1 DFMIQGGDF 9

Query Match 92.2%; Score 47; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 ADC17702
 ID ADC17702 standard; peptide; 9 AA.
 XX
 AC ADC17702;
 DT 18-DEC-2003 (first entry)
 XX
 DE Cyclophilin B protein amino acids 91-99.
 XX
 KW cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.
 XX
 OS Synthetic.
 XX
 PN WO2003020306-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002WO-JP008641.
 XX
 PR 29-AUG-2001; 2001JP-00260046.
 XX
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Yamada A;
 XX
 DR WPI; 2003-300831/29.
 XX
 PT Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.
 XX
 PS Claim 8; SEQ ID NO 2; 49pp; Japanese.
 XX
 CC The invention relates to allergic reaction suppressors, comprising a
 CC peptide which originates from the same antigenic substance as the
 CC antigenic substance inducing the (peptide-originated) allergic reaction,
 CC and containing an epitope different from the epitope participating in the
 CC induction of the allergic reaction and yet does not induce the allergic
 CC reaction. The desensitizers or allergic reaction suppressors are useful
 CC for treating and preventing type I allergic diseases and in cancer
 CC vaccines for preventing or treating cancer. The allergic reaction
 CC suppressors are also useful for suppressing an allergic reaction or
 CC reducing immunoglobulin E antibody production, and for desensitization to
 CC antigens. This sequence represents a peptide used in the invention and
 CC corresponds to amino acids 91-99 of the cyclophilin B protein.
 XX
 SQ Sequence 9 AA;
 Query Match 92.2%; Score 47; DB 7; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYMIQGGDF 9
 DB 1 DFMIOGGDF 9
 RESULT 10
 ADG89642
 ID ADG89642 standard; peptide; 9 AA.
 XX
 AC ADG89642;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Class I HLA-restricted widely expressed antigen #7.
 XX
 KW metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; widely antigen.

XX Unidentified.
 OS
 PN WO2003100027-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-MAY-2003; 2003WO-US016736.
 XX
 PR 28-MAY-2002; 2002US-0383530P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI; 2004-035134/03.
 XX
 PT Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.
 XX
 PS Disclosure; SEQ ID NO 85; 137pp; English.
 XX
 CC The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted widely expressed
 CC antigen.
 XX
 SQ Sequence 9 AA;
 Query Match 92.2%; Score 47; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYMIQGGDF 9
 DB 1 DFMIOGGDF 9
 RESULT 11
 AAY69958
 ID AAY69958 standard; peptide; 9 AA.
 XX
 AC AAY69958;
 XX
 DT 11-APR-2000 (first entry)
 XX
 DE Human cyclophilin B peptide fragment #38.
 XX
 KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 OS
 PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMI) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.
 XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.

```

XX PS Claim 4; Page 61; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 9 AA;
    Query Match      80.4%; Score 41; DB 3; Length 9;
    Best Local Similarity 87.5%; Pred. No. 1.7e+06;
    Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYMIQGGD 8
   |:|||||
Db 1 DFMIQGGD 8

RESULT 12
AA69961
ID AAY69961 standard; peptide; 9 AA.
AC AAY69961;
DT 11-APR-2000 (first entry)
XX Human cyclophilin B peptide fragment #41.
DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 2 /label= Phe, Tyr, Met, Trp
FT Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met
FT Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met
XX WO9967288-A1.
XX 29-DEC-1999.
XX 24-JUN-1999; 99WO-JP003360.
XX 25-JUN-1998; 98JP-00178449.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITOH/) ITOH K.
XX Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX diagnosis of tumors.
XX Claim 10; Page 60; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B, that
XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 9 AA;
    Query Match      72.5%; Score 37; DB 3; Length 9;
    Best Local Similarity 87.5%; Pred. No. 1.7e+06;
    Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DYMIQGGD 8
   |:|||||
   FN WO9611949-A2.

```

```

Db 1 DXMIQGGD 8

RESULT 13
AA69957
ID AAY69957 standard; peptide; 9 AA.
XX AAY69957;
AC AAY69957;
DT 11-APR-2000 (first entry)
XX Human cyclophilin B peptide fragment #37.
DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX Homo sapiens.
XX WO9967288-A1.
XX 29-DEC-1999.
XX 24-JUN-1999; 99WO-JP003360.
XX 25-JUN-1998; 98JP-00178449.
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITOH/) ITOH K.
XX Itoh K, Gomi S;
XX WPI; 2000-116932/10.
XX Tumor antigen peptides derived from cyclophilin B for treatment and
XX diagnosis of tumors.
XX Claim 4; Page 61; 64pp; Japanese.
XX This sequence represents a cyclophilin B peptide of the invention. The
XX peptides are tumour antigen peptides derived from cyclophilin B, that
XX recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 9 AA;
    Query Match      70.6%; Score 36; DB 3; Length 9;
    Best Local Similarity 75.0%; Pred. No. 1.7e+06;
    Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YMIQGGDF 9
   |:|||||
Db 2 FMCQGGDF 9

RESULT 14
AAR91898
ID AAR91898 standard; protein; 12 AA.
XX AAR91898;
AC AAR91898;
DT 03-DEC-1996 (first entry)
XX KGF-b minor component N-terminal fragment.
DE Keratinocyte growth factor; KGF; Cys1; Cys15; deletion; substitution;
KW Met-KGF analog; stimulate; non-fibroblast epithelial cell; antibody;
KW sebaceous gland; burn; burn; gastric ulcer; duodenal ulcer; liver function;
KW hepatic cirrhosis; ss.
XX Synthetic.
XX WO9611949-A2.

```

```

XX 25-APR-1996.
XX 12-OCT-1995; 95WO-IB000971.
XX 13-OCT-1994; 94US-00323340.
XX 13-OCT-1994; 94US-00323475.
XX 07-JUN-1995; 95US-00487825.
XX (AMGE-) AMGEN INC.
XX Morris CF, Kenney WC, Chen B, Hsu EW;
XX WPI; 1996-221944/22.
XX Keratinocyte growth factor analogues with modified N-terminal region -
XX stimulate prodn. of non-fibroblast epithelial cells and are useful e.g.
XX to treat gastric and duodenal ulcers.
XX Example 3; Page 52; 118pp; English.
XX The sequences given in AAR91897-98 represent the N-terminal peptides from
XX the major and minor components, KGF-a and KGF-b, of recombinantly
XX expressed keratinocyte growth factor (KGF). Interestingly the N-terminal
XX fragment of KGF-b indicates that it is an N-terminally truncated form of
XX KGF which is proteolytically cleaved at the Arg23-Ser24 peptide bond. KGF
XX may be used in the construction of KGF analogues (see also AAR91865-96).
XX These analogues have up to the first 24 N-terminal amino acids modified
XX so that Cys1 and Cys15 are deleted or substituted. Deleting or
XX substituting the Cys residues at positions 1 and 15 of native KGF
XX produces a KGF analogue which has substantially improved stability. These
XX KGF analogues can be used to stimulate the production of non-fibroblast
XX epithelial cells. They are useful as therapeutic, diagnostic and research
XX agents and in the generation of antibodies for the detection or
XX purification of native KGF. The KGF analogues may be applied to tissues
XX with damage to, or insufficient numbers of, non-fibroblast epithelium
XX cells. This includes the stimulation, proliferation and differentiation
XX of adnexal structures, e.g. hair follicles, sweat glands, and sebaceous
XX glands in burns patients, treating gastric and duodenal ulcers, and
XX increasing liver function to treat or prevent e.g. hepatic cirrhosis
XX
XX Sequence 12 AA;
  Query Match      53.9%; Score 27.5; DB 2; Length 12;
  Best Local Similarity 75.0%; Pred. No. 2.4e+02;
  Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DYMIQGGD 8
   ||| :|||
Db 3 DYM-EGGD 9

RESULT 15
AAR45361
ID AAR45361 standard; peptide; 9 AA.
XX
AC AAR45361;
XX
XX 16-OCT-2003 (revised)
DT 04-JUL-1994 (first entry)
XX
XX Choline oxidase N-terminal.
XX
XX Preparation; high; purity; yield; chemical analysis; esterase;
KW determination; phospholipid.
XX
XX Saccharomonospora glauca.
XX
XX JP05317056-A.
XX
XX 03-DEC-1993.
XX
XX 22-JAN-1993; 93JP-00008835.

```

```

XX 22-JAN-1992; 92JP-00009256.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX WPI; 1994-011021/02.
XX DNA fragment for choline oxidase prepn., for high purity and high yield -
XX comprises gene coding choline oxidase prepd. by culturing microbe
XX transformed by recombinant plasmid for choline chemical analysis and
XX choline esterase determ.
XX Claim 5; Page 2; 8pp; Japanese.
XX The sequence is that of the N-terminal of choline oxidase. Choline
XX oxidase is useful for chemical analysis of choline, determination of
XX choline esterase contained in serum and determination of phospholipid.
XX (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 9 AA;
  Query Match      52.9%; Score 27; DB 2; Length 9;
  Best Local Similarity 57.1%; Pred. No. 1.7e+06;
  Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYMIQGG 7
   ||| :|||
Db 3 DIVVGGG 9

Search completed: October 21, 2004, 07:21:04
Job time : 84 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:13:10 ; Search time 21.5 Seconds

(without alignments)
27.761 Million cell updates/sec

Title: US-09-720-469A-40

Perfect score: 51

Sequence: 1 DYM1QGDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	49.0	9	1	US-08-457-172-1
2	25	49.0	12	2	US-08-406-330-75
3	25	49.0	12	2	US-08-556-597-75
4	24	47.1	8	2	US-08-459-568-75
5	24	47.1	8	2	US-08-399-411-75
6	24	47.1	8	3	US-08-516-859A-75
7	24	47.1	8	3	US-09-586-472-75
8	24	47.1	8	4	US-09-528-706-75
9	24	47.1	10	3	US-08-765-953-8
10	24	47.1	10	6	5196404-18
11	24	47.1	10	6	5433940-25
12	24	47.1	12	4	US-09-846-350A-1
13	23.5	46.1	11	1	US-07-620-426B-19
14	23.5	46.1	11	1	US-07-662-007B-19
15	23.5	46.1	11	1	US-07-824-247-19
16	23.5	46.1	11	3	US-08-470-204A-19
17	23	45.1	8	1	US-08-487-860-62
18	23	45.1	10	1	US-08-658-130-21
19	23	45.1	10	5	PCT-US96-08723-21
20	23	45.1	12	3	US-09-188-579-51
21	23	45.1	12	3	US-09-329-350-27
22	23	45.1	12	3	US-09-315-444-51
23	23	45.1	12	4	US-09-721-362-51
24	23	45.1	12	4	US-09-752-165-71
25	23	45.1	12	4	US-08-841-636A-27
26	22	43.1	8	1	US-08-266-514-17
27	22	43.1	8	2	US-08-654-604-17

28 22 43.1 9 1 US-08-215-805A-7
29 22 43.1 9 1 US-08-215-805A-52
30 22 43.1 9 1 US-08-215-805A-58
31 22 43.1 9 2 US-08-637-759B-444
32 22 43.1 9 3 US-08-871-355A-444
33 22 43.1 9 3 US-09-201-945-444
34 22 43.1 11 3 US-09-026-276-23
35 22 43.1 11 4 US-09-964-201A-23
36 22 43.1 12 1 US-08-082-849B-15
37 22 43.1 12 4 US-09-785-921A-13
38 22 43.1 12 5 PCT-US94-01624-15
39 21.5 42.2 9 1 US-08-410-941-17
40 21.5 42.2 9 1 US-08-468-546-17
41 21.5 42.2 9 2 US-08-468-547-17
42 21.5 42.2 9 2 US-08-467-937-17
43 21.5 42.2 9 3 US-09-074-950-17
44 21.5 42.2 9 4 US-09-573-068-17
45 21.5 42.2 12 1 US-08-410-941-11

ALIGNMENTS

RESULT 1
US-08-457-172-1
; Sequence 1, Application US/08457172
; Patent No. 5622837
; GENERAL INFORMATION:
; APPLICANT: Hans Scheefers, Ursula Scheefers-Borchel and
; APPLICANT: Andreas Sziegoleit
; TITLE OF INVENTION: PANCREAS ELASTASE 1-SPECIFIC ANTIBODY, A PROCESS FOR
; TITLE OF INVENTION: OBTAINING IT, AND A TEST KIT CONTAINING SUCH ANTIBODY
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,172
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,395
; FILING DATE:
; APPLICATION NUMBER: US 07/969,173
; FILING DATE: 29-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42883/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: pancreatic
US-08-457-172-1

Query Match 49.0%; Score 25; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY 3 YMIQGD 8
| : |||
Db 2 MVAGGD 7

RESULT 2
US-08-406-330-75
; Sequence 75, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-75

Query Match 49.0%; Score 25; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0;

QY 2 YMIQGGDF 9
| : |||
Db 1 FVVRGGTF 8

RESULT 3
US-08-556-597-75
; Sequence 75, Application US/08556597
; Patent No. 587155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-75

Query Match 49.0%; Score 25; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 YMIQGGDF 9
| : |||
Db 1 FVVRGGTF 8

RESULT 4
US-08-459-568-75
; Sequence 75, Application US/08459568
; Patent No. 581304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1264
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-568-75

Query Match 47.1%; Score 24; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIQGGD 8
Db 3 LLEGGD 8

RESULT 5

US-08-399-411-75
Sequence 75, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-399-411-75

Query Match 47.1%; Score 24; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIQGGD 8
Db 3 LLEGGD 8

RESULT 6

US-08-516-859A-75
Sequence 75, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:

APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-75

Query Match 47.1%; Score 24; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIQGGD 8
Db 3 LLEGGD 8

RESULT 7

US-09-586-472-75
Sequence 75, Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000

```
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/528,706
; FILING DATE: 17-MAR-2000
; APPLICATION NUMBER: US 08/516,859
; FILING DATE: 18-AUG-1995
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 4130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-586-472-75
Query Match 47.1%; Score 24; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MIQGGD 8
Db 3 LLEGGD 8

RESULT 8
US-09-528-706-75
; Sequence 75, Application US/09528706
; Patent No. 6468985
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/528,706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/516,859
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 75:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-528-706-75
Query Match 47.1%; Score 24; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MIQGGD 8
Db 3 LLEGGD 8

RESULT 9
US-08-765-953-8
; Sequence 8, Application US/08765953
; Patent No. 6342201
; GENERAL INFORMATION:
; APPLICANT: DINKELBORG, LUDGER
; APPLICANT: STEPHAN, CHRISTOPH
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: SPECK, ULRICH
; APPLICANT: KENKLEIN, PETER
; TITLE OF INVENTION: COMPLEX COMPOUNDS FOR DIAGNOSIS OF
; TITLE OF INVENTION: VASCULAR DISEASES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK & MORTIMER
; STREET: 500 West Madison Street, Suite 3800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60661-2511
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: COMPAQ Prolinea 4/25s
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect for Windows 6.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,953
; FILING DATE: 17-JULY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE95/00837
; FILING DATE: 21-JUNE-1995
; APPLICATION NUMBER: P 44 25 778.3
; FILING DATE: 13-JULY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mortimer, John S.
; REGISTRATION NUMBER: 30,407
; REFERENCE/DOCKET NUMBER: 1214.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/876-1800
; TELEFAX: 312/876-2020
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-765-953-8
Query Match 47.1%; Score 24; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 6 GGDF 9
    ||||
Db 1 GGDF 4

RESULT 10
5196404-18
; Patent No. 5196404
; APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/549,388
; FILING DATE: 06-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO:18:
; LENGTH: 10
5196404-18

Query Match 47.1%; Score 24; DB 6; Length 10;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIQGG 7
    ||::||
Db 2 DFLAEGG 8

RESULT 11
5433940-25
; Patent No. 5433940
; APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
; TITLE OF INVENTION: INHIBITORS OF THROMBIN
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,259
; FILING DATE: 17-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 548,388
; FILING DATE: 06-JUL-1989
; APPLICATION NUMBER: 395,482
; FILING DATE: 18-AUG-1989
; SEQ ID NO:25:
; LENGTH: 10
5433940-25

Query Match 47.1%; Score 24; DB 6; Length 10;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

Qy 1 DYMIQGG 7
    ||::||
Db 2 DFLAEGG 8

RESULT 12
US-09-846-350A-1
; Sequence 1, Application US/09846350A
; Patent No. 6599877
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; APPLICANT: Marshall, John
; APPLICANT: Vrees, Tammy
; APPLICANT: Thatcher, Brad
; TITLE OF INVENTION: Biopolymer Marker Indicative Of Disease State Having A Molecular
; FILE REFERENCE: of 1020 Daltons
; FILE REFERENCE: 2132.025
; CURRENT APPLICATION NUMBER: US/09/846,350A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-350A-1

Query Match 47.1%; Score 24; DB 4; Length 12;
Best Local Similarity 42.9%; Pred. No. 2.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIQGG 7
    ||::||
Db 2 DFLAEGG 8

RESULT 13
US-07-620-426B-19
; Sequence 19, Application US/07620426B
; Patent No. 5298421
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Maelor
; APPLICANT: Pollard, Michael Roman
; APPLICANT: Voekler, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/620,426B
; FILING DATE: 19901130
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APRIL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 70-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-620-426B-19

Query Match 46.1%; Score 23.5; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DYMIQGG 7
    |||||
Db 1 DY-IQGG 6

RESULT 14
US-07-662-007B-19
; Sequence 19, Application US/07662007B
```

Patent No. 5344771
GENERAL INFORMATION:
APPLICANT: Davies, Huw Maelor
APPLICANT: Pollard, Michael Roman
APPLICANT: Voelker, Toni Alois
APPLICANT: Thompson, Gregory A.
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: MicrosoftWord 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/662,007B
FILING DATE: 19910408
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/514,030
FILING DATE: 26-APR-1990
APPLICATION NUMBER: 07/620,426
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: CGNE 70-2
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-662-007B-19

Query Match 46.1%; Score 23.5; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 DYMIQGG 7
Db 1 DY-IQGG 6

RESULT 15
US-07-824-247-19
Sequence 19, Application US/07824247
Patent No. 5512482
GENERAL INFORMATION:
APPLICANT: Voelker, Toni Alois
TITLE OF INVENTION: Plant Thioesterases
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: MicrosoftWord 4.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/824,247
FILING DATE: 19920122
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,263
FILING DATE: 24-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/773,096
FILING DATE: 7-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/704,861
FILING DATE: 21-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02960
FILING DATE: 25-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,007
FILING DATE: 27-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,426
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/514,030
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: CGNE 82-3
TELEPHONE: 916-753-6313
TELEFAX: 916-753-1510
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-824-247-19

Query Match 46.1%; Score 23.5; DB 1; Length 11;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 DYMIQGG 7
Db 1 DY-IQGG 6

Search completed: October 21, 2004, 07:29:31
Job time : 22.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:15:25 ; Search time 61.75 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-09-720-469A-40

Perfect score: 51

Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 193469

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	16 US-10-788-016-9	Sequence 9, Appli
2	47	92.2	9	15 US-10-447-161-85	Sequence 85, Appl
3	47	92.2	9	16 US-10-788-016-2	Sequence 2, Appli
4	26	51.0	10	10 US-09-573-822C-257	Sequence 257, App
5	26	51.0	12	14 US-10-320-231A-18	Sequence 18, Appl
6	25	49.0	9	15 US-10-057-475B-10856	Sequence 10856, A
7	25	49.0	9	15 US-10-057-475B-10911	Sequence 10911, A
8	25	49.0	9	15 US-10-154-884B-10856	Sequence 10856, A
9	25	49.0	9	15 US-10-154-884B-10911	Sequence 10911, A
10	25	49.0	9	15 US-10-363-791-103	Sequence 103, App
11	25	49.0	9	15 US-10-182-252A-872	Sequence 872, App
12	24	47.1	10	9 US-09-846-350-1	Sequence 1, Appli
13	24	47.1	11	9 US-09-846-342-1	Sequence 1, Appli
14	24	47.1	11	15 US-10-356-257-161	Sequence 161, App

15	24	47.1	12	9	US-09-845-725-1	Sequence 1, Appli
16	23	45.1	9	15	US-10-182-252A-281	Sequence 281, App
17	23	45.1	9	15	US-10-182-252A-282	Sequence 282, App
18	23	45.1	9	15	US-10-182-252A-878	Sequence 878, App
19	23	45.1	9	15	US-10-182-252A-879	Sequence 879, App
20	23	45.1	9	15	US-10-182-252A-880	Sequence 880, App
21	23	45.1	9	15	US-10-182-252A-881	Sequence 881, App
22	23	45.1	9	15	US-10-182-252A-882	Sequence 882, App
23	23	45.1	9	15	US-10-182-252A-883	Sequence 883, App
24	23	45.1	11	9	US-09-791-378-497	Sequence 497, App
25	23	45.1	11	9	US-09-791-378-546	Sequence 546, App
26	23	45.1	11	9	US-09-791-378-583	Sequence 583, App
27	23	45.1	11	9	US-09-826-290-337	Sequence 337, App
28	23	45.1	11	10	US-09-791-393-216	Sequence 216, App
29	23	45.1	11	10	US-09-791-389-216	Sequence 216, App
30	23	45.1	11	11	US-09-791-377-497	Sequence 497, App
31	23	45.1	11	11	US-09-791-377-546	Sequence 546, App
32	23	45.1	11	11	US-09-791-377-583	Sequence 583, App
33	23	45.1	11	14	US-10-076-047A-55	Sequence 55, Appl
34	23	45.1	11	15	US-10-264-309-466	Sequence 466, App
35	23	45.1	12	8	US-08-841-636A-27	Sequence 27, Appl
36	23	45.1	12	14	US-10-167-831-71	Sequence 71, Appl
37	23	45.1	12	16	US-10-782-002-27	Sequence 27, Appl
38	23	45.1	12	16	US-10-825-378-27	Sequence 891, App
39	22	43.1	9	15	US-10-182-252A-891	Sequence 891, App
40	22	43.1	9	15	US-10-182-252A-892	Sequence 892, App
41	22	43.1	9	15	US-10-182-252A-893	Sequence 893, App
42	22	43.1	9	15	US-10-182-252A-894	Sequence 894, App
43	22	43.1	9	15	US-10-182-252A-895	Sequence 895, App
44	22	43.1	9	15	US-10-182-252A-896	Sequence 896, App
45	22	43.1	9	15	US-10-182-252A-897	Sequence 897, App

ALIGNMENTS

RESULT 1

US-10-788-016-9
; Sequence 9, Application US/10788016
; Publication No. US2004014192A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788, 016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid residues from the 91st residue to the 99th residue of
; OTHER INFORMATION: cyclophilin B
US-10-788-016-9

Query Match 100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQGGDF 9

Db 1 DYMIQGGDF 9

RESULT 2

US-10-447-161-85

; Sequence 85, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-85

Query Match 92.2%; Score 47; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIOGGDF 9
:|||||
Db 1 DFMIOGGDF 9

RESULT 3

US-10-788-016-2
; Sequence 2, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
; OTHER INFORMATION: to the 99th residue of cyclophilin B
US-10-788-016-2

Query Match 92.2%; Score 47; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIOGGDF 9
:|||||
Db 1 DFMIOGGDF 9

RESULT 4

US-09-573-822C-257
; Sequence 257, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 257
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG024 at 351-360 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-573-822C-257

Query Match 51.0%; Score 26; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYMIOGGD 8
:||||
Db 1 NYLIKDGD 8

RESULT 5

US-10-320-231A-18
; Sequence 18, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-18

Query Match 51.0%; Score 26; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YMIOGGDF 9
:||||
Db 3 YFLYNGDF 10

RESULT 6

US-10-057-475B-10856
; Sequence 10856, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01440205
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22

;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 10979
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10856
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Lyl484 long MHC HLA A2 class I binding peptide
US-10-057-475B-10856

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGGDF 9
:|||||
Db 2 LQGSF 7

RESULT 7
US-10-057-475B-10911
;; Sequence 10911, Application US/10057475B
;; Publication No. US20040002068A1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; APPLICANT: Clapper, Jonathan David
;; APPLICANT: Wang, Aijun
;; APPLICANT: Ordenez, Nadia
;; APPLICANT: Carter, Lauren
;; APPLICANT: McNeill, Patricia Dianne
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;; FILE REFERENCE: 014058-014402US
;; CURRENT APPLICATION NUMBER: US/10/057,475B
;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 11290
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10856
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Lyl484 long MHC HLA A2 class I binding peptide
US-10-154-884B-10856

Query Match 49.0%; Score 25; DB 15; Length 9;

;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 10979
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10911
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Lyl484 short MHC HLA A2 class I binding peptide
US-10-057-475B-10911

Query Match 49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGGDF 9
:|||||
Db 2 LQGSF 7

RESULT 8
US-10-154-884B-10856
;; Sequence 10856, Application US/10154884B
;; Publication No. US20040005561A1
;; GENERAL INFORMATION:
;; APPLICANT: Gaiger, Alexander
;; APPLICANT: Algate, Paul A.
;; APPLICANT: Mannion, Jane
;; APPLICANT: Retter, Marc W.
;; APPLICANT: Corixa Corporation
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;; FILE REFERENCE: 014058-013521US
;; CURRENT APPLICATION NUMBER: US/10/154,884B
;; CURRENT FILING DATE: 2002-05-23
;; PRIOR APPLICATION NUMBER: US 60/186,126
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US 60/190,479
;; PRIOR FILING DATE: 2000-03-17
;; PRIOR APPLICATION NUMBER: US 60/200,545
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: US 60/200,303
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,779
;; PRIOR FILING DATE: 2000-04-28
;; PRIOR APPLICATION NUMBER: US 60/200,999
;; PRIOR FILING DATE: 2000-05-01
;; PRIOR APPLICATION NUMBER: US 60/202,084
;; PRIOR FILING DATE: 2000-05-04
;; PRIOR APPLICATION NUMBER: US 60/206,201
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: US 60/218,950
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 11290
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10856
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Lyl484 long MHC HLA A2 class I binding peptide
US-10-154-884B-10856

Query Match 49.0%; Score 25; DB 15; Length 9;

```
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000-274218
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-103

Query Match      49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DYMIQGDF 9
Db      1 DITIYGND 9

RESULT 11
US-10-182-252A-872
; Sequence 872, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 330307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/000059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 872
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-872

Query Match      49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 MIQGDF 9
Db      1 MIQGNF 7

RESULT 12
US-09-846-350-1
; Sequence 1, Application US/09846350
; Patent No. US20020161188A1
; GENERAL INFORMATION:
; APPLICANT: JACKOWSKI, GEORGE
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1020 DALTONS
; FILE REFERENCE: 2132.025
; CURRENT APPLICATION NUMBER: US/09/846,350
```

```
; FILE REFERENCE: 66.7%; Pred. No. 1.2e+06;
; CURRENT APPLICATION NUMBER: 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 IQGGDF 9
Db      2 LQGGSF 7

RESULT 9
US-10-154-884B-10911
; Sequence 10911, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: GAIGER, ALEXANDER
; APPLICANT: ALGATE, PAUL A.
; APPLICANT: MANNION, JANE
; APPLICANT: RETTER, MARC W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10911
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-154-884B-10911

Query Match      49.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 IQGGDF 9
Db      2 LQGGSF 7

RESULT 10
US-10-363-791-103
; Sequence 103, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, MASATO
; APPLICANT: KUZUMAKI, NO. US20040029197A10RU
; APPLICANT: SATO, NO. US20040029197A11YUKI
; APPLICANT: SAHARA, HIROEKI
; TITLE OF INVENTION: A NOVEL HUMAN CANCER/TESTIS-ASSOCIATED GENE THEREOF
```

```
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-350-1

Query Match          47.1%; Score 24; DB 9; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYMIQGG 7
       |:::||
Db      1 DFLAEGG 7

RESULT 13
US-09-846-342-1
; Sequence 1, Application US/09846342
; Patent No. US20020160422A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.026
; CURRENT APPLICATION NUMBER: US/09/846,342
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-342-1

Query Match          47.1%; Score 24; DB 9; Length 11;
Best Local Similarity 42.9%; Pred. No. 9.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYMIQGG 7
       |:::||
Db      2 DFLAEGG 8

RESULT 14
US-10-356-257-161
; Sequence 161, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-161

Query Match          47.1%; Score 24; DB 15; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 YMIQGG 7
```

```
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match          47.1%; Score 24; DB 9; Length 12;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYMIQGG 7
       |:::||
Db      3 DFLAEGG 9

RESULT 15
US-09-845-725-1
; Sequence 1, Application US/09845725
; Patent No. US20020161185A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match          47.1%; Score 24; DB 9; Length 12;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 DYMIQGG 7
       |:::||
Db      3 DFLAEGG 9

Search completed: October 21, 2004, 07:33:43
Job time : 61.75 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:12:54 ; Search time 15.75 Seconds
(without alignments)
54.981 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	45.1	11	2 B60769	Ig H2 chain - Paci
2	20	39.2	10	2 E60589	sperm-activating p
3	20	39.2	12	2 A61309	glycoprotein hormo
4	20	39.2	12	2 PH1458	T-cell receptor be
5	20	39.2	12	2 S43170	kinesin light chai
6	19	37.3	10	2 PN0165	triose-phosphate i
7	19	37.3	10	2 F33932	Ig mu chain J regi
8	19	37.3	11	2 PU0029	33K protein 3218 -
9	19	37.3	12	2 S65730	hemoglobin, extrac
10	18	35.3	7	2 PT0542	T-cell receptor be
11	18	35.3	8	2 PQ0012	cholecystokinin -
12	18	35.3	8	2 A43001	cholecystokinin -
13	18	35.3	8	2 JS0318	leucokinin VIII -
14	18	35.3	9	2 QDRB	delta sleep-induci
15	18	35.3	11	2 PT0250	Ig heavy chain CRD
16	18	35.3	11	2 PH1343	Ig heavy chain DJ
17	18	35.3	11	2 S60354	retinal oxidase -
18	18	35.3	11	2 PN0044	protein kinase C i
19	18	35.3	11	2 PT0218	T-cell receptor be
20	18	35.3	11	2 I41946	Trimeresurus serin
21	18	35.3	11	2 A61575	T-cell receptor be
22	18	35.3	12	2 S26544	T-cell receptor be
23	17	33.3	3	3 A23751	spinal cord peptid
24	17	33.3	9	1 YFPG	thymic factor - pi
25	17	33.3	9	2 A60957	thymocyte growth p
26	17	33.3	10	2 E41946	T-cell receptor ga
27	17	33.3	10	2 A60589	sperm-activating p
28	17	33.3	11	2 S57575	T cell receptor V-
29	17	33.3	11	2 D37196	bradykinin-potenti

30	17	33.3	11	4 S19015	hypothetical prote
31	16	31.4	9	2 E41978	calli:EMEPamide 5 -
32	16	31.4	9	2 F41978	calli:EMEPamide 6 -
33	16	31.4	9	2 G41978	calli:EMEPamide 7 -
34	16	31.4	10	2 C61440	polygalacturonase
35	16	31.4	10	2 S62880	monodehydroascorba
36	16	31.4	10	2 A44871	sperm-activating p
37	16	31.4	10	2 C60787	sperm-activating p
38	16	31.4	10	2 A60588	sperm-activating p
39	16	31.4	10	2 C60527	sperm-activating p
40	16	31.4	10	2 E39572	sperm-activating p
41	16	31.4	10	2 D60589	T-cell receptor be
42	16	31.4	12	2 S26541	Ig H chain V-D-J r
43	16	31.4	12	2 PH1606	Z protein - guinea
44	16	31.4	12	2 S23168	hypothetical prote
45	16	31.4	12	2 T46794	

ALIGNMENTS

RESULT 1

B60769
Ig H2 chain - Pacific hagfish (fragment)
C:Species: Eptatretus stouti (Pacific hagfish)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C:Accession: B60769
R:Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A:Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A:Reference number: A60769; MUID:91060965; PMID:2123225
A:Accession: B60769
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HAN>

Query Match 45.1%; Score 23; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQ 5
DB 5 DPMIQ 9

RESULT 2

E60589
sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I) - Echinometa mathaei
C:Species: Echinometa mathaei
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: E60589
R:Yoshino, K.I.; Kajiuira, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.; Yoshino, K.I.; Kajiuira, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides from Echinometa mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: E60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7M4C1
A>Note: an identical peptide was isolated from Echinometa mathaei type A and type B

Query Match 39.2%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YMIQGG 7
DB 2 YLSGG 7

RESULT 3

A61309

glycoprotein hormones alpha chain - hamster (fragment)
 N;Alternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lutr
 C;Species: Criceinae gen. sp. (hamster)
 C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
 C;Accession: A61309
 R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.
 Endocrinology 111, 1263-1269, 1982
 A;Title: Isolation and characterization of hamster luteinizing hormone.
 A;Reference number: A61309; MUID:83003498; PMID:6889489
 A;Accession: A61309
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <GLS>
 A;Cross-references: UNIPROT:Q7M0A7
 C;Superfamily: Glycoprotein hormones alpha chain
 C;Keywords: glycoprotein

Query Match 39.2%; Score 20; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIQG 6
 | : : :
 Db 5 DFTMQG 10

RESULT 4
 PH1458
 T-cell receptor beta chain (clone 332/1K) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
 C;Accession: PH1458; S26543
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib
 A;Reference number: PH1430; MUID:93171821; PMID:8436911
 A;Accession: PH1458
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 A;Experimental source: cytolytic T-lymphocyte, clone 332/1K
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A;Reference number: S26512; MUID:92364546; PMID:1380061
 A;Accession: S26543
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <CA2>
 A;Cross-references: EMBL:X67993
 A;Experimental source: cytolytic T-lymphocyte, clone Cw3/C44
 C;Keywords: receptor; T-cell

Query Match 39.2%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QGGDF 9
 | : : :
 Db 5 QGSDY 9

RESULT 5
 S43170
 kinesin light chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C;Accession: S43170
 R;Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
 submitted to the EMBL Data Library, December 1992
 A;Description: Promoter first exon/intron characterization and chromosomal location of t
 A;Reference number: S43170
 A;Accession: S43170
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-12 <CH>
 A;Cross-references: UNIPROT:Q13865; EMBL:X69658; NID:G468786; PIDN:CAA49349.1; PID:G468786

Query Match 39.2%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MIQGG 7
 | : : :
 Db 1 MLRGG 5

RESULT 6
 PN0165
 triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: PN0165
 R;Fukaya, N.; Chow, L.P.; Sugliura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A;Reference number: PN0160
 A;Accession: PN0165
 A;Molecule type: protein
 A;Residues: 1-10 <FUK>
 A;Cross-references: UNIPROT:Q7M4X7
 A;Experimental source: strain M-1-1
 C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 37.3%; Score 19; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGDF 9
 | : : :
 Db 7 GGNF 10

RESULT 7
 F33932
 Ig mu chain J region (E7) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
 C;Accession: F33932
 R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l
 A;Reference number: A33932; MUID:89282823; PMID:2499867
 A;Accession: F33932
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-10 <BAC>
 A;Cross-references: UNIPROT:Q99NG4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q1; UNIP
 ROT:Q9DCD9; UNIPROT:Q924R0; UNIPROT:Q8K172; UNIPROT:Q99LA6; UNIPROT:Q91X92; GB:M27106
 C;Keywords: immunoglobulin

Query Match 37.3%; Score 19; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYMIQG 6
 | : : :
 Db 3 DYWGQG 8

RESULT 8
 PU0029
 33K protein 3218 - rice (strain Nohonbare) (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 C;Accession: PU0029
 R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A:Reference number: PS0208

A:Accession: PU0029

A:Molecule type: protein

A:Residues: 1-11 <TSU>

A:Experimental source: bran

C:Comment: molecular weight 33K, pI 6.0.

Query Match 37.3%; Score 19; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QGGDF 9

Db 3 EGGPF 7

RESULT 9

S65730

hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)

C:Species: Lumbricus terrestris (common earthworm)

C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C:Accession: S65730

R:Pushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.

Biochim. Biophys. Acta 1292, 273-280, 1996

A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin

A:Reference number: S65721; MUID:96176855; PMID:8597573

A:Accession: S65730

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <FUS>

Query Match

Best Local Similarity 37.3%; Score 19; DB 2; Length 12;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIIQ 5

Db 7 DHLIQ 11

RESULT 10

PT0542

T-cell receptor beta chain V-D-J region (126-LBA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0542

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0542

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-7 <FEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 35.3%; Score 18; DB 2; Length 7;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8

Db 3 GGD 5

RESULT 11

PQ0012

cholecystokinin - southeastern quoll

N:Alternate names: CCK

C:Species: Dasyurus viverrinus (southeastern quoll)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: PQ0012

R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.

Peptides 9, 429-431, 1988

A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.

A:Reference number: PQ0012; MUID:88234141; PMID:3375140

A:Accession: PQ0012

A:Molecule type: protein

A:Residues: 1-8 <FAN>

A:Cross-references: UNIPROT:P30369

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein

F;2/Binding site: sulfate (Tyr) (covalent) #status predicted

F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 35.3%; Score 18; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYM 3

Db 1 DYM 3

RESULT 12

A43001

cholecystokinin - tammar wallaby

N:Alternate names: CCK

C:Species: Macropus eugenii (tammar wallaby)

C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 09-Jul-2004

C:Accession: A43001; PQ0012

R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.

Peptides 9, 429-431, 1988

A:Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.

A:Reference number: PQ0012; MUID:88234141; PMID:3375140

A:Accession: A43001

A:Molecule type: protein

A:Residues: 1-8 <FAN>

A:Cross-references: UNIPROT:P30369

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein

F;2/Binding site: sulfate (Tyr) (covalent) #status predicted

F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match

Best Local Similarity 35.3%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYM 3

Db 1 DYM 3

RESULT 13

JS0318

leucokinin VIII - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: JS0318

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the final

A:Reference number: JS0317

A:Accession: JS0318

A:Molecule type: protein

A:Residues: 1-8 <HOL>

A:Cross-references: UNIPROT:P19990

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile acti

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 35.3%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGDF 9
|
Db 1 GADF 4

RESULT 14

QDRB

delta sleep-inducing peptide - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C/Accession: A01422
R/Monnier, M.; Dudler, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.A.
Experientia 33, 548-552, 1977
A/Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original
A/Reference number: A01422; MUID:77185324; PMID:862769
A/Accession: A01422
A/Molecule type: protein
A/Residues: 1-9 <MON>
A/Cross-references: UNIPROT:P01158
C/Comment: This peptide was obtained from dialysates of occipital venous sinus blood from
of recipient rabbits, it induces spindle and delta EEG activity and reduced motor activity

Query Match 35.3%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGD 8
|
Db 3 GGD 5

RESULT 15

PT0250

Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0250
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0250
A/Molecule type: DNA
A/Residues: 1-11 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 35.3%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GDF 9
|
Db 4 GDF 6

Search completed: October 21, 2004, 07:28:00
Job time : 16.75 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2004, 07:05:04 ; Search time 86 Seconds
(without alignments)
60.214 Million cell updates/sec

Title: US-09-720-469A-40
Perfect score: 51
Sequence: 1 DYMTQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	45.1	7	Q63480	Q63480 rattus norv
2	22	43.1	9	Q9PS68	Q9PS68 gallus gall
3	22	43.1	12	Q9H3W2	Q9H3W2 homo sapien
4	21	41.2	11	Q70Y64	Q70Y64 plectranthu
5	21	41.2	11	CAD45529	CAD45529 plectranth
6	21	41.2	12	Q70Y58	Q70Y58 clinopodium
7	21	41.2	12	CAD45546	CAD45546 clinopodi
8	20	39.2	8	Q70Y88	Q70Y88 platostoma
9	20	39.2	8	CAD45489	CAD45489 platostom
10	20	39.2	10	Q7M4C1	Q7M4C1 echinometra
11	20	39.2	12	Q13865	Q13865 homo sapien
12	20	39.2	12	Q7M0A7	Q7M0A7 cricetidae
13	19	37.3	7	O55184	O55184 rattus norv
14	19	37.3	10	Q7M4X7	Q7M4X7 fusarium sp
15	19	37.3	10	Q8UWV2	Q8UWV2 oreochromis
16	19	37.3	11	Q9HFN8	Q9HFN8 candida rug
17	19	37.3	11	Q77876	Q77876 oreochromis
18	19	37.3	11	Q70Y98	Q70Y98 capitaniopsi
19	19	37.3	11	CAD45456	CAD45456 capitaniop
20	19	37.3	12	Q8UUV8	Q8UUV8 squalus aca
21	19	37.3	12	Q8UUV0	Q8UUV0 rana catesb
22	18	35.3	8	CKKN MACEU	P30369 macropus eu
23	18	35.3	8	LCK8 LEUMA	P19990 leucophaea
24	18	35.3	8	LMT2 LOEMI	P22396 locusta mig
25	18	35.3	8	Q9TT78	Q9TT78 canis famil
26	18	35.3	9	DSIF RABIT	P01158 cryptotagus
27	18	35.3	9	Q6LDH6	Q6LDH6 rattus norv
28	18	35.3	9	AAA40600	AAA40600 rattus no
29	18	35.3	10	Q51812	Q51812 plasmodi f.
30	18	35.3	11	Q87882	Q87882 mycobacteri
31	18	35.3	11	P83168	P83168 struthio ca

Q9n2b8 pongo pygma
Q9n2b9 gorilla gor
Q9n2c0 Pan troglod
Q46712 plasmid r10
P81012 schizaphis
P84071 allium asca
Q90zv5 fulica leuc
P01255 sus scrofa
Q7m3c5 ovis aries
P81731 helicoverpa
Q6ic14 homo sapien
Q96ga7 homo sapien
Q7m4b7 heterocentr
Q8mj52 equus cabal

32 18 35.3 12 2 Q9N2B8
33 18 35.3 12 2 Q9N2B9
34 18 35.3 12 2 Q9N2C0
35 18 35.3 12 2 Q46712
36 17.5 34.3 10 1 ESTA SCHGA
37 17 33.3 7 1 ASCL ALLAS
38 17 33.3 8 2 Q90ZV5
39 17 33.3 9 1 THVF PIG
40 17 33.3 9 2 Q7M3C5
41 17 33.3 10 1 AMPN HELAM
42 17 33.3 10 2 Q6LCI4
43 17 33.3 10 2 Q96QA7
44 17 33.3 10 2 Q7M4B7
45 17 33.3 10 2 Q8MJ52

ALIGNMENTS

RESULT 1
Q63480 PRELIMINARY; PRT; 7 AA.
ID Q63480
AC Q63480;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RT Endocrinology 137:1562-1571(1996).
RL EMBL; U59125; AAB02827.1;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;
Query Match 45.1%; Score 23; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. NO. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 IQGGD 8
Db 2 IRGGD 6
RESULT 2
Q9PS68 PRELIMINARY; PRT; 9 AA.
ID Q9PS68
AC Q9PS68;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE LOW density lipoprotein receptor-related protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92011685; PubMed=1918027;
RA Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,

RA Schneider W.J.;
 RT "The laying hen expresses two different low density lipoprotein
 receptor-related proteins";
 RL J. Biol. Chem. 266:19079-19087(1991).
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1039 MW; 895EC68B5AB2CDC1 CRC64;

Query Match 43.1%; Score 22; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYMIQ 5
 |||:
 Db 5 DYMK 9

RESULT 3

ID Q9H3W2 PRELIMINARY; PRT; 12 AA.
 AC Q9H3W2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TRE17 protein.
 GN Name=TRE17 gene;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010310; PubMed=8406013;
 RA Ono M., Nakamura T., Hillova J., Hill M.;
 RT "Identification of novel sequences in the repertoire of hypervariable
 TRE17 genes from immortalized nonmalignant and malignant human
 keratinocytes.";
 RT Keratinocytes.";
 RL Gene 131:209-215(1993).
 RN [2]

SEQUENCE FROM N.A.

RP MEDLINE=93228825; PubMed=8471161;

RA Ono M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.;
 RT "Human TRE17 oncogene is generated from a family of homologous
 polymorphic sequences by single-base changes.";
 RL DNA Cell Biol. 12:107-118(1993).
 RN [3]

SEQUENCE FROM N.A.

RA Hillova J.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; X71371; CAC16150.1; -;
 SQ SEQUENCE 12 AA; 1252 MW; 6E17AFDE83ADD87B CRC64;

Query Match 43.1%; Score 22; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGD 8
 |||:
 Db 3 MVEGAD 8

RESULT 4

ID Q70Y64 PRELIMINARY; PRT; 11 AA.
 AC Q70Y64;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rp16;
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OG Chloroplast.

SEQUENCE FROM N.A.

RA Hillova J.;
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; X71371; CAC16150.1; -;
 SQ SEQUENCE 12 AA; 1252 MW; 6E17AFDE83ADD87B CRC64;

Query Match 43.1%; Score 22; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGD 8
 |||:
 Db 3 MVEGAD 8

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
 OX NCBI_TaxID=204208;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15019625;
 RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505409; CAD45529.1; -;
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1317 MW; D8D98CB3AB587866 CRC64;

Query Match 41.2%; Score 21; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YMIQGG 7
 |||:
 Db 1 YGFQGG 6

RESULT 5

ID CAD45529 PRELIMINARY; PRT; 11 AA.
 AC CAD45529;
 DT 14-MAR-2004 (TrEMBLrel. 27, Created)
 DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (fragment).
 GN RPS16.
 OS Plectranthus ciliatus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
 OX NCBI_TaxID=204208;
 RN [1]

SEQUENCE FROM N.A.

RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions.";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505409; CAD45529.1; -;
 KW Chloroplast; Ribosomal protein.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1317 MW; D8D98CB3AB587866 CRC64;

Query Match 41.2%; Score 21; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YMIQGG 7
 |||:
 Db 1 YGFQGG 6

RESULT 6

ID Q70Y58 PRELIMINARY; PRT; 12 AA.
 AC Q70Y58;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (fragment).
 GN Name=rp16;

```

OS Clinopodium vulgare subsp. arundanum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium.
OX NCBI_TaxID=204223;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505446; CAD45546.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1353 MW; D43D1B51AF587866 CRC64;

Query Match 41.2%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 IQGG 7
Db 4 IQGG 7

RESULT 7
CAD45546 PRELIMINARY; PRT; 12 AA.
ID CAD45546;
AC CAD45546;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS16.
OS Clinopodium vulgare subsp. arundanum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Lamiales; Lamiaceae; Nepetoideae; Nepeteae; Clinopodium;
OC Clinopodium vulgare.
OX NCBI_TaxID=204223;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505446; CAD45546.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1353 MW; D43D1B51AF587866 CRC64;

Query Match 41.2%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 IQGG 7
Db 4 IQGG 7

RESULT 8
Q70Y88 PRELIMINARY; PRT; 8 AA.
ID Q70Y88
AC Q70Y88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```

```

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rps16;
OS Platostoma fimbriatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.
OX NCBI_TaxID=204168;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505368; CAD45489.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BB4772 CRC64;

Query Match 39.2%; Score 20; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YMIQGG 7
Db 3 YTVPGG 8

RESULT 9
CAD45489 PRELIMINARY; PRT; 8 AA.
ID CAD45489
AC CAD45489;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN RPS16.
OS Platostoma fimbriatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Platostoma.
OX NCBI_TaxID=204168;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505368; CAD45489.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BB4772 CRC64;

Query Match 39.2%; Score 20; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YMIQGG 7
Db 3 YTVPGG 8

RESULT 10
Q7M4C1

```

```

DE Glycoprotein hormones alpha chain (Fragment).
OS Cricetidae sp. (Hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
NCBI_TaxID=36483;
RN [1]
RP SEQUENCE.
RX MEDLINE=83003498; PubMed=6889489;
RA Glenn S.D., Nahm H.S., Greenwald G.S., Ward D.N.;
RT "Isolation and characterization of hamster luteinizing hormone.";
RL Endocrinology 111:1263-1269(1982).
PIR: A61309; A61309.
FT NON TER 1
FT NON TER 12
SQ SEQUENCE 12 AA; 1280 MW; 94A63728AA81A9CA CRC64;

Query Match 39.2%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYMIOG 6
Db | : | |
5 DFTMOG 10

RESULT 13
O55184
ID O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orphan receptor TR4-NS (Fragment).
GN Name=TR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=9619847; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IOGGD 8
Db | | | |
2 IOGGD 6

RESULT 14
Q7M4X7

```

```

ID Q7M4X7 PRELIMINARY; PRT; 10 AA.
AC Q7M4X7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Triose-phosphate isomerase (EC 5.3.1.1) (Fragment).
OS Fusarium sporotrichoides.
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
CX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Fukaya N., Chow L.P., Sugiura Y., Tsugita A., Ueno Y., Tabuchi K.;
RL Submitted (MAY-1994) to the PIR data bank.
DR PIR; P0165; P0165.
DR GO; GO:0004807; F:triose-phosphate isomerase activity; IEA.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1142 MW; 590E4D7862C9C3 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGDF 9
DB 7 GGNF 10

RESULT 15
Q8UVW2 PRELIMINARY; PRT; 10 AA.
ID Q8UVW2;
AC Q8UVW2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AMPA receptor subunit 2 alpha (Fragment).
GN Name=Glur2a;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
CX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21617183; PubMed=11741603;
RA Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;
RT "Q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript
RT evolves no later than the appearance of cartilaginous fishes.";
RL FEBS Lett. 509:277-281(2001).
DR EMBL; AF350050; AAL57192.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1153 MW; 721A6E5AAB866C4 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 8.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YMIQGD 8
DB 1 FMRQGD 7

```

